COMPOSITIONS AND METHODS RELATING TO STOP-1

This application claims benefit from United States Provisional Application No. 60/463,656, filed April 16, 2003, which application is incorporated by reference herein in its entirety.

FIELD OF THE INVENTION

The present invention is directed to STOP-1 polypeptides, antibodies, nucleic acid molecules, antagonists, agonists, potentiators and compositions relating to STOP-1, and methods of making and using the same, including methods for diagnosing and treating of tumors in mammals. The present invention further relates to the diagnosis and treatment of disorders involving angiogenesis and vasculogenesis (e.g., cardiovascular as well as oncological disorders).

BACKGROUND AND INTRODUCTION OF THE INVENTION

Uncontrolled cell growth is the cause of many illnesses in a variety of cell types. For example, cancer occurs when there is an increase in the number of abnormal, or neoplastic, cells derived from a normal tissue that proliferate to form a tumor mass. The tumor cells often invade the adjacent tissues and can spread via the blood or lymphatic system to regional lymph nodes and to distant sites via a process called metastasis. In a cancerous growth, a cell proliferates under conditions in which normal cells would not grow. Cancer manifests itself in a wide variety of forms, characterized by different degrees of invasiveness and aggressiveness. Malignant tumors (cancers) are the second leading cause of death in the United States, after heart disease (Boring et al., *CA Cancel J. Clin.* 43:7 (1993)).

Much research has been devoted to discovering new treatments for cell proliferative disorders, such as cancer. Despite recent advances, there is a great need to identify and understand the role of new cellular targets for modulating cell proliferation and to develop alternative or more effective methods of treatment and therapeutic and diagnostic agents. There is also a need to develop alternative therapeutics and methods for treating specific cell types and for treating illnesses caused by or associated with abnormal cell proliferation, such as cancers. For example, desmoplasia is the hyperplasia of fibroblasts and disproportionate formation of fibrous connective tissue, especially in the stroma of carcinomas. Desmoplasia is a hallmark of tumor invasion and malignancy. Desmoid tumors and abdominal fibroids are nodules or relatively large masses of unusually firm scarlike connective tissue resulting from

active proliferation of fibroblasts, occurring most frequently in the abdominal muscles of women who have borne children; the fibroblasts infiltrate surrounding muscle and fascia.

In post-natal life, vasculogenesis (endothelial cells forming a primary tubular network) and angiogenesis (the growth or sprouting of new blood vessels from existing vessels) play critical roles in the pathophysiology of neoplastic disorder (Semenza, G.L., (2003) *Ann. Rev. Med.* 54:17-28). The distinction between vasculogenesis and angiogenesis is not absolute and they overlap (Ribatti, D et al., (2001) *Mech.Dev.* 100:157-163). Both require endothelial cell proliferation, migration, three-dimensional reorganization of newly formed aggregates and use simlar extracellular matrix adhesive mechanisms (Ribatti, *supra*). Use of anti-angiogenic therapies such as the antibody against vascular endothelial growth (VEGF) called Avastin have been shown to be useful in treating cancers.

Another cellular protein, referred to herein as STOP-1 or UNQ762, has been shown to be overexpressed in certain tumors (e.g., WO 01/163318, WO 01/68848, WO 02/00690, WO 02/08284, WO 02/16602, WO 02/42487). Polyclonal antibodies against STOP-1 have been reported (e.g., WO 02/42487). Although there has been some discussion of targeting STOP-1 to treat cancers and diseases associated with angiogenesis (e.g., WO 01/163318, WO 01/68848, WO 02/00690, WO 02/08284, WO 02/16602, WO 02/42487, WO 00/71581, WO 02/00690), there is a need to further explore the biology of the STOP-1 protein to identify alternative and more effective therapeutic agents and methods for diagnosis and treatment of uncontrolled cell growth and diseases caused by, associated with or complicated by excessive and insufficient angiogenesis.

The present invention addresses these needs and others by providing new STOP-1 polypeptides, antibodies, nucleic acid molecules, compositions and methods that incorporate further knowledge about the STOP-1 protein. Among other things, the present disclosure shows that STOP-1 is overexpressed in the stroma of several tumor types. The present disclosure shows that overexpression of STOP-1 alone can be tumorigenic. Further, the present disclosure demonstrates that the STOP-1 protein can be secreted and that secretion is required for tumorigenesis. Still further, the present disclosure shows that the glycosylation state of STOP-1 affects whether it is secreted and that elimination of a N-glycosylation site, e.g., by substituting the amino acid at position 186 (Asn) with alanine results in loss of secretion. The present disclosure shows that disulfide bonding between STOP-1 proteins can occur at a cysteine 55 in culture in the triple helix domain of STOP-1. Additionally, the present disclosure shows that the STOP-1 protein can form a complex with itself as a dimer, trimer and hexamer and that the c-terminus of the protein is sufficient for oligomerization,

whereas a region related to the triple helix domain of collagen is not required. The present disclosure also shows a plurality of agents that specifically bind to STOP-1, including the C-terminal region and N-terminal region of the protein as well as nucleic acid and protein sequences encoding them. Further, the present disclosure shows that STOP-1 expression can be modulated by overexpression of proteins in the WNT signalling pathway that are know to cause breast cancer in mice, e.g., the overexpression of WNT. Additionally, the present disclosure shows that STOP-1 can be cleaved by proteases that are overexpressed in the same tumors as STOP-1, e.g., MMP-9. Further, the present disclosure shows that a method for producing STOP-1 polypeptides by expressing the polypeptides in proteoglycan synthesis deficient cell lines. The present invention shows that STOP-1 binds to the surface of cells, such as cancer cells and endothelial cells. The present invention provides antagonistic molecules that can inhibit the interaction of STOP-1 with the surface of cells. The present invention provides molecules that can potentiate the binding of STOP-1 with the surface of cells. The present invention also relates to the role of STOP-1 in angiogenesis and vasculogenesis and methods and compositions for treating disorders for which treatment would be improved by modulating angiogenesis and vasculogenesis. This data and others provided herein, together with other disclosure of in present application, teach new, better and/or alternative methods for using the STOP-1 protein or compositions relating thereto.

SUMMARY OF THE INVENTION

The present invention provides new therapeutic agents, diagnostic agents and methods for treating or preventing uncontrolled cell proliferation, including cancer, and other diseases by targeting the activity, expression and regulation of STOP-1. The present invention provides new therapeutic agents, diagnostic agents and methods for treatinga any medical condition having suboptimal, excessive or inappropriate angiogenic or vasculogenic events by targeting the activity, expression and regulation of STOP-1.

According to one embodiment, the present invention provides a monoclonal antibody that specifically binds to an oligomeric form of human STOP-1. According to another embodiment, the present invention provides, a monoclonal antibody that specifically binds to amino acids 33-53 or 33-52 of human STOP-1. In yet another embodiment, the present invention includes a monoclonal antibody that specifically binds to amino acids 94-243 of human STOP-1. According to further embodiment, the monoclonal antibody that specifically binds to residues 94-243 of human STOP-1 or residues 33-53 or 33-52 of human STOP-1 also recognizes an oligomeric form of human STOP-1, such as the trimeric form. An

antibody according to this invention can be isolated. It is understood that an aforementioned antibody that specifically binds a residue within residues 33-52 or 33-53 of human STOP-1 may also bind to other residues within STOP-1 or non-human equivalents thereof.

In yet another embodiment, the present invention provides monoclonal antibodies having the biological characteristics of an antibody selected from the group consisting of S7 encoded by the nucleic acid molecule deposited on March 25, 2003 as designation V0350-4-S7, S4 encoded by the nucleic acid molecule deposited on March 25, 2003 as designation V0350-2b-S4, S9 encoded by the nucleic acid molecule deposited on March 25, 2003 as designation V0350-2b-S9, S16 encoded by the nucleic acid molecule deposited on March 25, 2003 as designation V0350-4-S16, F5 encoded by the nucleic acid molecule deposited on March 25, 2003 as designation V0350-5 and 6B12 produced by the hybridoma cell line deposited on March 28, 2003 as designation 6B12.1.7 in the American Type Culture Collection (ATCC) , 10801 University Blvd., Manassas, VA 20110-2209, USA, including the deposited antibodies, antibodies comprising a portion of those antibodies and variants thereof. In another embodiment, the present invention provides antibodies that specifically bind to STOP-1, wherein the binding of the antibodies to STOP-1 can be inhibited (e.g., as observed in a competitive ELISA asay) by a second monoclonal antibody selected from one of the aforementioned deposited antibodies.

The present invention also relates to antibodies having the following sequences:

A monoclonal antibody comprising:

(a) a first amino acid sequence comprising:

T - I - X1 - X2- X3-X4

wherein X1 is S, N or T;
wherein X2 is G, N, S or A;
wherein X3 is Y, S or T; and
wherein X4 is D or W.

(b) a second amino acid sequence comprising:

X1-X2-I-X3-P-X4-X5-G-X6-T-X7 (SEQ ID NO:115)

wherein X1 is G or A;

wherein

(1) X2 is an amino acid selected from the group consisting of S, T, A, and X3 is an amino acid selected from the group consisting of R, W and Y; or

(2) X3 is an amino acid selected from the group consisting of S, T, A, and X2 is an amino acid selected from the group consisting of R, W and Y;

wherein X4 is Y or F;
wherein X5 is G, S, T or A;
wherein X6 is N, Y or A; and
wherein X7 is N, Y or D; and

(c) a third amino acid sequence comprising the sequence:

C-X1-X2-X3-G-G-X4-X5-X6-X7-X8-X9-X10-X11 (SEQ ID NO:116)

wherein X1 is A, S or T;
wherein X2 is basic amino acid;
wherein X3 is any amino acid;
wherein X4 is a hydrophobic amino acid;

wherein any one of X5- X8 can be any amino acid or can be missing, and at least one of X5-X8 is an aromatic amino acid or a hydrophobic amino acid;

wherein X9 is an aromatic or hydrophobic amino acid;
wherein X10 is D or A; and
wherein X11 is Y or V.

According to one embodiment, the monoclonal antibody comprises the light chain sequence of FIG.34. According to another embodiment, the monoclonal antibody is a full-length IgG.

According to one embodiment of this invention, the X1 of the first amino acid sequence is S. According to another embodiment of this invention, the X2 the first amino acid sequence is G. According to yet another embodiment of this invention, X3 of the first amino acid sequence is S. According to one embodiment, the first amino acid sequence is a sequence selected from the group consisting of TISGSD, TITNSD and TISGSW.

According to yet another embodiment of this invention, X3 of SEQ ID NO:115 is S or A. According to yet another embodiment of this invention, X4 of SEQ ID NO:115 is Y. According to yet another embodiment of this invention, X5 of SEQ ID NO:115 is G or A. According to yet another embodiment of this invention, X6 of SEQ ID NO:115 is N or A. According to one embodiment, SEQ ID NO:115 is a sequence selected from the group consisting of GRISPYGNTN, ATIYPYGGYTY and AWIAPYSGATD.

According to one embodiment of this invention, the X1 of SEQ ID NO:116 is A. According to another embodiment of this invention, the X2 of SEQ ID NO:116 is R. According to yet another embodiment of this invention, X4 of SEQ ID NO:116 is L or M. According to one preferred embodiment of this invention, the aromatic amino acid present in X5-X8 is a tryptophan residue. According to another embodiment, one amino acid of X5-X8 is missing. According to yet another embodiment of this invention, X9 of SEQ ID NO:116 is F. According to one embodiment of this invention, X10 of SEQ ID NO:116 is D. According to one embodiment of this invention, X11 of SEQ ID NO:116 is Y. According to one embodiment, the SEQ ID NO:116 is a sequence selected from the group consisting of CARVGGLKLLFDY, CARGGGMDGYVMDY and CAREGGLYWVFDY.

An antibody according to this invention can comprise (a) a first amino acid sequence comprising the sequence TISGSD; (b) a second amino acid sequence comprising the sequence GRISPYGNTN; and (c) a third amino acid sequence comprising the sequence CARVGGLKLLFDY, or a variant of said antibody. Alternatively, an antibody according to this invention can comprise (a) a first amino acid sequence comprising the sequence TITNSD; (b) a second amino acid sequence comprising the sequence ATIYPYGGYTY; and (c) a third amino acid sequence comprising the sequence CARGGGMDGYVMDY; or a variant of said antibody. Alternatively, an antibody according to this invention can comprise (a) a first amino acid sequence comprising the sequence TISGSW; (b) a second amino acid sequence comprising the sequence AWIAPYSGATD; and (c) a third amino acid sequence

comprising the sequence CAREGGLYWVFD; or a variant of said antibody. Alternatively, an antibody according to this invention can comprises (a) a first amino acid sequence comprising the sequence TISNYG; (b) a a second amino acid sequence comprising the sequence GRISPSNGSTY; and (c) a third amino acid sequence comprising the sequence CAKCSVRFAY; or a variant of said antibody. Alternatively, an antibody according to this invention can comprise (a) a first amino acid sequence comprising the sequence TINNYD; (b) a second amino acid sequence comprising the sequence GYISPPSGATY; and (c) third amino acid sequence comprising the sequence CARMVGMRRGVMDY; or a variant of said antibody.

In a further embodiment, the first, second and third amino acid sequences described above are located in a human heavy chain wherein the first amino acid sequence is at residues 28-33 of the heavy chain according to the Kabat numbering system, the second amino acid sequence is at residues 49-58 of the heavy chain according to the Kabat numbering system and the third amino acid sequence is at residues 92-102 according to the Kabat numbering system.

In another embodiment, the present invention provides a monoclonal antibody comprising the amino acid sequence of: (a) the heavy chain sequence of FIG.27; (b) the heavy chain sequence of FIG.28; (c) the heavy chain sequence of FIG.29; (d) the heavy chain sequence of FIG.30; (e) the heavy chain sequence of FIG.31; or (f) the heavy chain sequence of FIG.34; or variants thereof. In a further embodiment, the antibodies of this invention further comprise (a) the light chain sequence of FIG.27, (b) the light chain sequence of FIG.34; or variants thereof.

In a further embodiment, the antibodies of this invention are chimeric or humanized antibodies. In another embodiment, the antibodies of this invention are antibody fragments. In yet another embodiment of this invention, the antibodies are conjugated to an agent selected from the group consisting of a stromal targeting agent, a growth inhibitory agent, a cytotoxic agent, a detection agent, an agent that improves the bioavailability and an agent that improves the half-life of the antibody. In another embodiment, the antibody of this invention is a multi-specific antibody having a binding specificity for a STOP-1 polypeptide and one or more binding specificities for any other antigen. According to one embodiment, the other antigen is a cell-surface protein or receptor or receptor subunit. According to one preferred embodiment, the cell-surface protein is a natural killer (NK) receptor receptor. According to a more preferred embodiment, the binding of the antibody to the NK receptor activates the natural killer cell.

The present invention provides variants and modifications of STOP-1 polypeptide variants. In one embodiment, the STOP-1 polypeptide variant that cannot be secreted from a cell. In another embodiment, said variant is a human STOP-1 polypeptide that is not glycosylated. In a further embodiment, the variant is a human STOP-1 polypeptide that is mutated at residue 186. The present invention also provides a STOP-1 variant polypeptide comprising STOP-1 that cannot disulfide bind with another STOP-1. According to one embodiment, the variant is a human STOP-1 polypeptide that is mutated at residue 55.

The present invention also provides nucleic acid molecules encoding the antibodies and polypeptides and variants thereof, vectors comprising the nucleic acid molecules, and host cells comprising the nucleic acid molecules of this invention.

The present invention includes compositions comprising an antibody, a polypeptide or a nucleic acid molecule of this invention. According to one embodiment, the composition further comprises a pharmaceutically acceptable carrier. In a further embodiment, the composition comprises a stromal targeting agent. In a further embodiment, the stromal targeting agent is covalently linked to the monoclonal antibody or polypeptide. In yet a further embodiment, the stromal targeting agent recognizes a stromal cell of a tumor.

The present invention provides methods for producing a STOP-1 polypeptide or an anti-STOP-1 antibody of this invention by culturing a cell comprising a nucleic acid according to this invention. According to one embodiment, the method for producing a STOP-1 polypeptide comprises the step of culturing a mammalian cell that comprises a nucleic acid molecule encoding the STOP-1 polypeptide and that is deficient in proteoglycan synthesis. According to another embodiment, the cell line that is deficient in proteoglycan synthesis is deficient in galactosyltransferase I activity. According to one preferred embodiment, the cell line is a CHO-psbg cell line.

The present invention provides a method for determining the presence of a STOP-1 polypeptide in a sample comprising exposing a sample suspected of containing the STOP-1 polypeptide to an anti-STOP-1 antibody and determining binding of said antibody to a component of said sample. According to one embodiment, the antibody is a monoclonal antibody of this invention.

The present invention provides methods for diagnosing or monitoring a cell proliferative disorder, such as a tumor, of a patient comprising the step of comparing the expression of STOP-1 in a normal tissue to the amount of STOP-1 being tested from the patient. In one embodiment, a STOP-1 protein can be detected by an agent such as an antibody of this invention. In another embodiment, STOP-1 mRNA can be detected by an

agent such as a nucleic acid molecule that specifically hybridizes to the UNQ6762 mRNA. In a further embodiment, the tumor being tested has a large stromal compartment. In a further embodiment, STOP-1 detection agent is administered at or near the stromal compartment of the tissue being tested. In yet another embodiment, the method further comprises the step of observing or assaying the STOP-1 protein or mRNA in the stromal compartment agent of the normal tissue and tissue being tested. In another embodiment, the antibody is a monoclonal antibody of this invention.

The present invention provides a method of preventing or treating a proliferative disorder in a patient comprising the step of admininstering to the patient a composition of this invention in an amount effective to inhibit the proliferation of cells in the patient. In one embodiment, the proliferative disorder is desmoplasia. The present invention also provides a method of preventing or inhibiting the growth of a tumor that overexpresses STOP-1 in a patient comprising administering to the patient an antagonist of STOP-1 in an amount effective to inhibit growth of the tumor in the patient. In a further embodiment, the tumor to be treated has stromal compartments. In yet a further embodiment, the tumor having stromal compartments is selected from the group consisting of desmoid tumors, pancreatic cancer, sarcomas (e.g., hemangiosarcoma, rabdomyosarcoma) and adenocarcinomas (mammary adenocarcinomas, colon adenocarcinomas, gastrointestinal adenocarcinomas and ovarian adenocarcinomas), hepatocellular carcinoma, breast cancer, colon cancer, lung cancer, ovarian cancer, glioma, endometrial cancer and vascular cancer. In a further embodiment, the antagonist is administered at or near a stroma of the tumor. In another embodiment, the tumor is a melanoma or a round cell tumor (e.g., malignant fibrous hystiocytoma).

An antagonist according to this invention is any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native STOP-1 polypeptide and that specifically binds to a native STOP-1 polypeptide, wherein the binding of the antagonistic molecule (1) is to a native STOP-1 polypeptide in oligomeric form, (2) is to residues 94-243 of native human STOP-1 and/or (3) can be inhibited (e.g., as observed in a competitive ELISA assay using STOP-1 and 6B12) by a monoclonal antibody of this invention (e.g., a deposited antibody of this invention, etc.). According to one embodiment, the deposited antibody is the 6B12 antibody. According one embodiment, the antagonist is a polypeptide. According to another embodiment, the antagonist is an antibody of this invention. In another embodiment, the STOP-1 polypeptide that the antagonist inhibits is part of a trimeric complex.

According to another embodiment, the biological activity that is inhibited by the antagonist is the interaction of STOP-1 with a cell that specifically binds STOP-1. According to one embodiment, the cell is a breast cancer cell. According to another embodiment, the cell is an endothelial cell. According to yet another embodiment, the antagonist has an additional property selected from the group consisting of (1) capable of binding to an epitope within human STOP-1 that the 6B12 antibody binds; (2) capable of binding to a residue within at least residues 33-52 of human STOP-1; and (3) capable being competed from binding to STOP-1 by the 6B12 antibody (e.g., as observed in a competitive ELISA assay using STOP-1, the antagonist and the 6B12 antibody).

The present invention provides a method for inhibiting the growth of a cell that overexpresses STOP-1 comprising the step of inhibiting the secretion of STOP-1 from the cell. In one embodiment, secretion is inhibited by inhibiting glycosylation of STOP-1. In another embodiment, the secretion is inhibited by overexpressing a STOP-1 protein that cannot be secreted in the cell. In a further embodiment, the secretion is inhibited by a STOP-1 protein that is mutated at residue 186.

The present invention provides a method for preventing disulfide binding between STOP-1 molecules comprising a step selected from the group consisting of: (1) mutating STOP-1-encoding DNA molecules at residue cysteine 55; (2) expressing STOP-1 proteins that are mutated at residue cysteine 55 in the presence of naturally-occurring STOP-1 proteins; and (3) incubating STOP-1 proteins that are mutated at residue cysteine 55 with naturally-occurring STOP-1 proteins.

The present invention provides a method for cleaving STOP-1 comprising the step of incubating STOP-1 with a protease selected from the group consisting of a matrix metalloprotease-7 (MMP-7) and a matrix metalloprotease-9 (MMP-9). In a further embodiment, the method additionally comprises the step of monitoring the STOP-1 cleavage products produced.

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cell that overexpresses a STOP-1 polypeptide, wherein the method comprises administering an antagonist of STOP-1, wherein the antagonist specifically binds to STOP-1 and is optionally conjugated to one or a combination of the agent(s) selected from the group consisting of a stromal targeting agent, a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope and a nucleolytic enzyme. Another embodiment of the present invention is directed to a method for inhibiting the growth of a cell that overexpresses a STOP-1 polypeptide,

wherein the method comprises administering an agent to a stromal cell of the tumor, wherein the agent is an antagonist of STOP-1 or a nucleic acid molecule encoding a STOP polypeptide. The agent can be administered to the stromal cell directly by a patient or physician or indirectly, through the use of stromal targeting agents that can direct the agent to the stromal cell. The present invention provides an article of manufacture comprising (a) a composition of matter comprising a modified STOP-1 polypeptide, a STOP-1 polypeptide variant, STOP-1 antagonist, STOP-1 agonist, STOP-1 potentiator or a nucleic acid molecule encoding a STOP-1 polypeptide conjugated to a vehicle (e.g., such as antisense therapy or RNAi therapy); (b) a container containing said composition; and (c) a label affixed to said container, or a package insert included in said container referring to the use of said polypeptide variant, modified polypeptide or antagonist in the treatment of a proliferative disorder or a disease associated with abnormal angiogenesis or vasculogenesis (e.g., a package insert). According to one embodiment, the STOP-1 antagonist or potentiator is an antibody of this invention.

The present invention provides methods for testing the activity of STOP-1 and agonists or antagonists of STOP-1. In one embodiment, a method of inducing cell migration in vitro comprising administering to an endothelial cell a STOP-1 polypeptide in an amount effective to induce migration of said cell is provided. According to another embodiment, the present invention provides a method of testing the activity of a candidate antagonist or agonist of STOP-1 comprising the steps of treating a first endothelial cell with STOP-1, treating a second endothelial cell with STOP-1 and the candidate antagonist or agonist, and comparing the migration of the first and second endothelial cells. In one preferred embodiment, the cell used in such migration assay is a HUVEC cell.

The present invention also provides methods of treating a disease or condition associated with excessive, inappropriate or uncontrolled angiogenesis in a mammalian subject. In one embodiment, the method comprises the step of administering to the subject a STOP-1 antagonist in an amount effective to treat the disease, wherein the STOP-1 antagonist has any property selected from the group consisting of (1) binds to residues within human STOP-1 that the 6B12 antibody binds; (2) binds to a residue within at least residues 33-52 of human STOP-1; and (3) can be inhibited from binding to STOP-1 by the 6B12 antibody.

The present invention also contemplates treating patients who would benefit from increased angiogeneis vasculogenesis by administering a therapeutically effective amount of a STOP-1 potentiator, a molecule that enhances STOP-1 binding to cells and/or aggregates STOP-1 on the cell surface. Such a molecule would be administered in an amount effective

to increase angiogenesis or vasculogenesis. In one preferred embodiment, the agonist is an anti-STOP-1 antibody that aggregates STOP-1 a cell surface.

The present invention also provides agonists comprising an oligomeric form of STOP-1 polypeptide that comprises greater than three STOP-1 polypeptides. According to one embodiment the agonist comprises six STOP-1 polypeptides. According to another embodiment, the STOP-1 polypeptide is part of an immunoadhesin that is used to form said agonist.

The present invention provides new methods for identifying and evaluating candidate and know STOP-1 antagonists, agonist and potentiators comprising the step of observing or measuring the binding of STOP-1 to a cell in the presence and absence of the antagonist, agonist or potentiator. According to one embodiment, the cell is a cancer cell. In a further embodiment the cell is a breast cancer cell. According to another embodiment, the cell is an endothelial cell.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG.1 shows an alignment of amino acid sequences encoding STOP-1 from a wide variety of species - human (SEQ ID NO:1), mouse (SEQ ID NO:3), rice fish (SEQ ID NO:4), zebrafish (SEQ ID NO:5) and chicken (SEQ ID NO:6). A consensus sequence is also provided. The arrow indicates a signal sequence cleavage site. Red indicates residues conserved in all species. Capitalized letters in the consensus sequence indicates residues that have been conserved throughout all species. Lower case letters in the consensus sequence indicate residues that are conserved in most species. Residues that that are not conserved in those species appear as a "period." "!" indicates I or V. "$" indicates L or M. " %" indicates F or Y. "#" indicates B, D, E, N, Q or Z.

FIG.2 shows a nucleic acid sequence encoding human STOP-1. A signal sequence is indicated by the boxed amino acids. A triple helix domain is indicated by an underline. A glycosylation site is at amino acid 186.

FIG.3 shows (A) the presence of human STOP-1 mRNA in certain tissue types and (B) mouse STOP-1 mRNA from different stages of mouse development. Full length human or mouse STOP-1 DNAs were radiolabelled and used to probe northern blots of tissues from adult humans or developing mouse embryos.

FIG.4 shows coomassie-stained human STOP-1 proteins produced by (A) CHO-DP12 or (B) CHO-psgb (ATCC) cells and purified by nickel-NTA affinity chromatography. The vector, pRK5, was used as a control.

FIG.5 shows a western blot of human histidine-tagged STOP-1 protein present in the (A) supernatant and (B) cell lysate of transient transfected CHO-psgb cells. The western blot was probed with anti-his antibody.

FIG.6 shows the oligomerization of human STOP-1 protein expressed using a baculoviral infection system in SF9 insect cells. STOP-1 protein and various deletion mutants were expressed from SF9 cells, separated on a size exclusion column and subjected to light scattering analysis e.g., (A) S31-K243, (B) E89-K243 and (C) L94-K243. The predicted molecular weight of the monomers appear in the left corner of each graph. The numbers appearing next to several peaks refer to the average molecular weight of the complexes in the peak

FIG.7 shows the oligomerization of human STOP-1 protein expressed from mammalian cells. Human STOP-1 protein and various deletion mutants were expressed from CHO cells, separated on a size exclusion column and subjected to light scattering analysis, e.g., (A) M1-K243 and (B) delta-THD (residues 1-54, 94-243, plus histidine tag). The predicted molecular weight of the monomers appear in the left corner of each graph. The numbers appearing next to several peaks refer to an average molecular weight of the complexes in those peaks. Under non-reducing conditions, western blots of secreted full length, his-tagged human STOP-1 protein recombinantly expressed from CHO-psgb cells presented predominantly homodimerized complexes (C). The western blots were probed with anti-his antibody.

FIG.8 shows western blots of (A) cell culture media and (B) whole cell lysates from CHO-psgb cells expressing human his-tagged STOP-1 WT, delta-THD, and delta-delta-THD STOP-1 (residues 1-51, 94-243, plus histidine tag) and subjected to reducing or non-reducing conditions. The western blots were probed with anti-his antibody.

FIG.9 shows western blots of (A) cell culture media and (B) whole cell lysates from CHO-psgb cells expressing his-tagged WT, G53A and N186A STOP-1 constructs and subjected to reducing or non-reducing conditions. The western blots were probed with anti-his antibody.

FIG.10 shows western blots of (A) cell culture media and (B) whole cell lysates from CHO-psgb cells expressing his-tagged WT, C55A, C93A and C109A STOP-1 constructs and subjected to reducing or non-reducing conditions. The western blots were probed with anti-his antibody.

FIG.11 shows that murine STOP-1 mRNA (mSTOP-1 mRNA) is expressed in breast tumors derived from MMTV-WNT1 transgenic mice but not in normal mammary epithelial cells. RNA samples were taken from breast tumor cells (marked "T1"-"T7") or C57Mg mouse normal mammary epithelial cells (marked, "N"), subjected to RT-PCR with mSTOP-1 primers and mRLP19 primers. The PCR products were separated on an agarose gel.

FIG.12 shows the proliferation of 3T3 cells after transfection with (A) human STOP-1 or (B) mouse STOP-1. FIG.12A shows the amount of ^{3}H-thymidine incorporation (counts per minute (cpm)) in 3T3 cells at 12, 28 and 96 hours after addition of of ^{3}H-thymidine. FIG.12B shows the amount of ^{3}H-thymidine incorporation (counts per minute (cpm)) in 3T3 cells at 12, 28 and 96 hours after addition of ^{3}H-thymidine. Controls: transfections with vector alone (puro2 and ph1).

FIG.13 shows the proliferation of 3T3 or 293 cells after infection with retrovirus encoding human STOP-1. FIG.13A and B are western blots of human STOP-1 proteins expressed from 3T3 cells or 293, respectively, infected with a retrovirus encoding a control vector (Babe) or human STOP-1. STOP-1 was immunoprecipitated from whole cell lysates using the S7-IgG antibody. Western blots were probed with polyclonal anti-human STOP-1 antibodies. FIG.13C shows the level of cell proliferation observed for the infected cell populations as detected by a colorimetric Cell Titer Assay.

FIG.14 shows that mouse STOP-1 promotes tumorigenesis by 3T3 fibroblasts in a xenograft mouse model. FIG.14A shows the mean volume of tumors in mice implanted with 3T3 fibroblasts transfected with vector alone (p2 vector) or DNA encoding mouse STOP-1 or

RAS protein. The transfected cells were implanted into nude mice or tested for protein expression. FIG.14B and C show western blots of aliquots of the supernatants and lysates, respectively, of the transfected cells. The western blot was probed with rabbit anti-STOP-1 polyclonal antibodies. "TI" refers to the tumor incident ratio.

FIG.15 shows that human STOP-1 promotes tumorigenesis by 3T3 fibroblasts in a xenograft mouse model. FIG.15 shows the mean tumor volume of tumors in mice implanted with 3T3 fibroblasts transfected with vector alone or DNA encoding human STOP-1, RAS protein or LP1.

FIG.16 shows that recombinant STOP-1 protein potentiates SK-Mel-31 cells wound healing and motility. SK-Mel-31 cells were treated with (A) NT – no exogenous ligand treatment, (B) b762 – baculoviral produced human STOP-1 protein, (C) hrEGF – (50 ng/ml), (D) hrEGF and b762 or (E) CHO mammalian produced human STOP-1 protein.

FIG.17 shows that anti-human STOP-1 antibody, 6B12, binds to the N-terminal sequence of human STOP-1 between the signal sequence and triple helix domains. FIG.17A is a schematic of the his-tagged human and full length zebrafish STOP-1 proteins used in the epitope location studies of FIGs.18B and C. FIG.17B and C show western blots probed with anti-his antibody and 6B12 antibody, respectively, of extracts from cells that recombinantly expressed the proteins of FIG.17A.

FIG.18 shows the amino acid sequences of the CDRs of several phage-derived antibodies having affinity for human STOP-1. "H1," "H2" and "H3" refer to V_H-CDR1, V_H-CDR2 and V_H-CDR3. The numerical header generally corresponds to amino acid positions 28-33, 49-58 and 92-102 according to the Kabat numbering system.

FIG.19 shows a graph of an ELISA assay to determine an optimal concentration of S4 and S7 Fab or IgG for use in a competition ELISA to determine the affinity of the antibodies for STOP-1. "S coated" refers to a short form (#94-243) of STOP-1 coated on a microtiter plate. "F coated" refers to a full-length form of human STOP-1 coated on a microtiter plate. Approximately 90% of maximal binding was considered to be optimal for use in a competitive ELISA assay. Horse-radish peroxidase-conjugated protein G was used to detect the bound Fab and IgG.

FIG.20 shows a graph of the results of competitive ELISA to determine the binding affinities of the S4 and S7 Fab or IgG. The plates were coated with short form or full-length human STOP-1 and competed with short form or full length STOP-1, respectively (FIG.20A and B, respectively). The calculated binding affinities are indicated in the parentheticals.

FIG.21 shows a summary of the binding affinities of several phage-derived antibodies against STOP-1. "S/S" refers to an ELISA in which the microtiter plate was coated with a short form of STOP-1 and competed with a short form of STOP-1. "F/S" refers to an ELISA in which the microtiter plate was coated with a full-length form of human STOP-1 and competed with a short form of human STOP-1. "F/F" refers to an ELISA in which the microtiter plate was coated with a full-length form of STOP-1 and competed with a full-length form of STOP-1. The phage used in these studies were the S4-Fab phage and the S7-$F(ab)'_2$ phage.

FIG.22 shows a graph of an ELISA assay in which the plates were coated with human STOP-1, bound with S4 IgG and then competed with S4 (Fab) phage, S7 ($F(ab)'_2$) phage, S9 (Fab) phage, S16 ($F(ab)'_2$) phage and F5 ($F(ab)'_2$) phage. The Y axis refers to percentage unblocked as calculated by dividing the OD450nm value of the well that blocked S4 IgG by the OD450nm value of a well without S4 IgG.

FIG.23 shows a coomassie stained gel of baculovirus-expressed human STOP-1 protein cleaved by various proteases *in vitro*. "MMP" refers to matrix metalloprotease.

FIG.24A-D are schematics of phagemids encoding Fab of $F(ab)'_2$ phage display proteins or vectors encoding Fab or IgG proteins. FIG.24A is a schematic of a Fab-phagemid construct. The construct contains an alkaline phosphatase promoter, an STII signal sequence, a V_L and C_L light chain sequence, a gD tag, another STII signal sequence, a heavy chain V_H and CH_1 region and a C-terminal part of the M13 bacteriophage pIII coat protein (cP3). FIG.24B is a schematic of a $F(ab)'_2$-phagemid construct. The construct contains generally the same sequences as the Fab-phagemid, except it additionally includes a leucine zipper sequence (Zip). FIG.24C is a schematic of a nucleic acid molecule encoding a Fab protein. FIG.24D is a schematic of a nucleic acid molecule encoding an IgG protein, which IgG protein includes a CH_2 and CH_3 sequence.

FIG.25A-H describe amino acid sequences and a nucleic acid sequence for a phage display anti-Her-2 Fab. More specifically, FIG.25 shows an amino acid sequence comprising an anti-Her-2 Fab light chain (SEQ ID NO:86), an amino acid sequence comprising an anti-Her-2 Fab light chain region (SEQ ID NO:87) and the nucleic acid sequence of a phagemid encoding the amino acid sequences (SEQ ID NO:88).

FIG.26A-H describe amino acid sequences and a nucleic acid sequence for a phage display anti-Her-2 F(ab)'$_2$. More specifically, FIG.26 shows an amino acid sequence comprising an anti-Her-2 F(ab)'$_2$ light chain (SEQ ID NO:89), an amino acid sequence comprising an anti-Her-2 F(ab)'$_2$ heavy chain region (SEQ ID NO:90) and the nucleic acid sequence of a phagemid encoding the amino acid sequences (SEQ ID NO:91).

FIG.27A-C describe amino acid sequences and a nucleic acid sequence for a phage display S4-Fab. More specifically, FIG.27 shows an amino acid sequence comprising an S4-Fab light chain (SEQ ID NO:92), an amino acid sequence comprising an S4-Fab heavy chain region (SEQ ID NO:93) and a nucleic acid sequence encoding the amino acid sequences (SEQ ID NO:94).

FIG.28A-C describe amino acid sequences and a nucleic acid sequence for a phage display S9 Fab. More specifically, FIG.28 shows an amino acid sequence comprising an S9-Fab light chain (SEQ ID NO:95), an amino acid sequence comprising an S9-Fab heavy chain region (SEQ ID NO:96) and a nucleic acid sequence encoding the amino acid sequences (SEQ ID NO:97).

FIG.29A-C describe amino acid sequences and a nucleic acid sequence for a phage display S7-F(ab)'$_2$. More specifically, FIG.29 shows an amino acid sequence comprising an S7-F(ab)'$_2$ light chain (SEQ ID NO:98), an amino acid sequence comprising an S7-F(ab)'$_2$ heavy chain region (SEQ ID NO:99) and a nucleic acid sequence encoding the amino acid sequences (SEQ ID NO:100).

FIG.30A-C describe amino acid sequences and a nucleic acid sequence for a phage display S16-F(ab)'$_2$. More specifically, FIG.30 shows an amino acid sequence comprising an S16-F(ab)'$_2$ light chain (SEQ ID NO:101), an amino acid sequence comprising an S16-

F(ab)'$_2$ heavy chain region (SEQ ID NO:102) and a nucleic acid sequence encoding the amino acid sequences (SEQ ID NO:103).

FIG.31A-C describe amino acid sequences and a nucleic acid sequence for a phage display F5-F(ab)'$_2$. FIG.31 shows an amino acid sequence comprising a F5-F(ab)'$_2$ light chain (SEQ ID NO:104), an amino acid sequence comprising an F5-F(ab)'$_2$ heavy chain region (SEQ ID NO:105) and a nucleic acid sequence encoding the amino acid sequences(SEQ ID NO:106).

FIG.32A-G describe amino acid sequences and a nucleic acid sequence for a S4-Fab. More specifically, FIG.32 shows an amino acid sequence comprising an S4-Fab light chain (SEQ ID NO:107), an amino acid sequence comprising an S4-Fab heavy chain region (SEQ ID NO:108) and the nucleic acid sequence of a vector encoding the amino acid sequence (SEQ ID NO:109).

FIG.33A-F describe an S4 light chain sequence of an IgG protein. More specifically, FIG.33 shows an amino acid sequence comprising an S4 Light Chain (SEQ ID NO:110) and the nucleic acid sequence of a vector encoding the amino acid sequence (SEQ ID NO:111).

FIG.34A-G describe an S4 heavy chain sequence of an IgG protein. More specifically, FIG.34 shows an amino acid sequence comprising an S4 Heavy Chain (SEQ ID NO:112) and the nucleic acid sequence of a vector encoding the amino acid sequence (SEQ ID NO:113).

FIG.35 shows a frequency of amino acids in human antibody light chain sequences from the Kabat database.

FIG.36 shows one illustrative embodiment of a suitable codon set design.

FIG.37 is an illustrative embodiment of restricted diversity degenerate (also referred to herein as "nonrandom") codon sets for diversification of CDRs L1, L2 & L3.

FIG.38 is an illustrative embodiment of restricted diversity degenerate (also referred to herein as "nonrandom") codon sets for diversification of CDRs L1, L2 & L3.

FIG.39 is an illustrative embodiment of restricted diversity degenerate (also referred to herein as "nonrandom") codon sets for diversification of CDR L3.

FIG.40 is an illustrative embodiment of a restricted diversity degenerate (also referred to herein as "nonrandom") codon sets for diversification of CDRs L1, L2 & L3.

FIG.41 shows a flow cytometric analysis of populations of 293, HeLa, HT1080 or HUVEC cells treated with either (1) anti-HIS antibodies, (2) anti-HIS antibodies and STOP-1 protein or (3) anti-flag antibodies and STOP-1 protein, followed by treatment with fluorescein isothiocyanate (FITC)-conjugated goat anti-mouse antibodies. A small, insignificant number of cells bound the anti-flag antibodies (i.e., the peaks at far left corner of the x-axis in the 293, HeLa and HT1080 graphs). The x-axis indicates the number of cells (log fluorescein signal intensity). The y-axis indicates the level of fluorescence emitted by the labeled cells (events).

FIG.42 shows a FACS analysis of populations of HT1080 cells treated with (1) anti-HIS antibodies, (2) anti-HIS antibodies and STOP-1 protein, (3) anti-flag antibodies and STOP-1 protein, (3) STOP-1 protein, (4) STOP-1 protein and S7 antibodies or (5) STOP-1 and 6b12 antibodies, followed by treatment with FITC-conjugated goat anti-mouse antibodies.

FIG.43 charts the migration of HT1080 cells (number of cells) in a modified Boyden chemotactic chamber after treatment with bFGF or STOP-1 ("762") or a negative control.

FIG.44 shows a FACS analysis of STOP-1 binding to MDA435 cells in the presence and absence of an anti-STOP-1 antibody (6B12) or an antibody control (4B7). The detection antibody, anti-flag M2 -FITC antibody, did not effect STOP-1 binding.

FIG.45 is a graph that shows the fold change in STOP-1 mRNA expression after treatment (A) under hypoxic conditions for 8 and 34 hours or (B) under normoxic conditions for 3, 8 and 34 hours, in the presence and absence of recombinant human TNFalpha.

DETAILED DESCRIPTION OF THE INVENTION

A nucleic acid sequence coding for a STOP-1 protein according to this invention includes, e.g., SEQ ID NO:1 and the nucleic acid molecules encoding the polypeptides of FIG.1.

SEQ ID NO:1

```
GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGG
CGGAGCCAGACGCTGACCACGTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTG
CCCGGCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCG
GCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCA
AGGGGAAGCAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT
GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTC
CGGGTACACCTGGGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGA
GGGAAAGCTTTGAGGAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGA
ATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATA
GTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC
AGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAGGACCTCTTCCCATTGAAGCTA
TAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTT
CTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTC
GCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTT
TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCT
GAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCACACTGTTTTTAA
ATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTT
AGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTGTGGTCT
TTTGTTTTTTCTCTTAGTATAGCATTTTTAAAAAAATATAAAAGCTACCAATCTTTGTAC
AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA
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The terms "STOP-1," "STOP-1 protein," "STOP-1 polypeptide" (also refered to UNQ762 or 762) as used herein include native sequence polypeptides, polypeptide variants and fragments of native sequence polypeptides and polypeptide variants (which are further defined herein), unless specified otherwise. STOP-1 proteins can be obtained from various species, e.g., humans, by using antibodies according to this invention or by recombinant or synthetic methods, including using deposited nucleic acid molecules. An oligomeric form of STOP-1 includes a human STOP-1 having only residues 94-243, or a part thereof. An oligomeric form according to this invention can include a dimer, a trimer and a hexamer of STOP-1. According to one preferred embodiment, the oligomeric form of STOP-1 is a trimer.

A "native sequence" polypeptide or "native" polypeptide is one which has the same amino acid sequence as a polypeptide (e.g., antibody) derived from nature. A "native sequence" polypeptide is one which has the same amino acid sequence as a polypeptide (e.g., antibody) derived from nature. Such native sequence polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. Thus, a native sequence polypeptide can have the amino acid sequence of a naturally occurring human polypeptide, murine polypeptide, or polypeptide from any other mammalian species. A "native sequence" STOP-1 polypeptide or a "native" STOP-1 polypeptide comprises a polypeptide having the

same amino acid sequence as the corresponding STOP-1 polypeptide derived from nature. For example, in one preferred embodiment, the nucleic acid sequence encoding a native sequence of human STOP-1 can be found in SEQ ID NO:2 and FIG.2.

SEQ ID NO:2
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQ
GPAGVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSL
NYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPI
EAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGW
NSVSRIIIEELPK

Such STOP-1 polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence" or "native" STOP-1 polypeptide or protein specifically encompasses naturally-occurring truncated or secreted forms of the STOP-1 protein, naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In certain embodiments of the invention, the native sequence STOP-1 polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures.

The approximate location of the "signal peptides" of the various STOP-1 polypeptides disclosed herein can be seen in the present specification and/or the accompanying figures. It is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"STOP-1 polypeptide variant" means a STOP-1 polypeptide having at least about 80% amino acid sequence identity with a full-length native sequence STOP-1 polypeptide sequence as disclosed herein, a STOP-1 polypeptide sequence lacking the signal peptide or triple helix domain as disclosed herein, or any other fragment of a full-length STOP-1 polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length STOP-1 polypeptide). Such STOP-1 polypeptide variants include, for instance, STOP-1 polypeptides wherein one or more amino acid residues are added, or deleted, at the N– or C-terminus of the full-length native amino acid sequence. Ordinarily, a STOP-1 polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%,

or 99% amino acid sequence identity, to a full-length native sequence STOP-1 polypeptide sequence as disclosed herein, a STOP-1 polypeptide sequence lacking the signal peptide as disclosed herein, a triple helix domain of a STOP-1 polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length STOP-1 polypeptide sequence as disclosed herein. Ordinarily, STOP-1 variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600 amino acids in length, or more. Optionally, STOP-1 variant polypeptides will have no more than one conservative amino acid substitution as compared to the native STOP-1 polypeptide sequence, alternatively no more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 conservative amino acid substitution as compared to the native STOP-1 polypeptide sequence.

"Percent (%) amino acid sequence identity" with respect to the STOP-1 polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific STOP-1 polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or can be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "STOP-1", wherein "STOP-1" represents the amino acid sequence of a hypothetical STOP-1 polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "STOP-1" polypeptide of interest is being compared, and "X, "Y" and "Z" each represent different hypothetical amino acid residues. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

"STOP-1 variant polynucleotide" or "STOP-1 variant nucleic acid sequence" means a nucleic acid molecule which encodes a STOP-1 polypeptide, preferably an active STOP-1 polypeptide, as defined herein and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence STOP-1 polypeptide sequence as disclosed herein, a full-length native sequence STOP-1 polypeptide sequence lacking the signal peptide as disclosed herein, the triple helix domain of a STOP-1 polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length STOP-1 polypeptide sequence as disclosed herein (e.g., residues 94-243 of human STOP-1). Ordinarily, a STOP-1 variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence STOP-1

polypeptide sequence as disclosed herein, a full-length native sequence STOP-1 polypeptide sequence lacking the signal peptide as disclosed herein, the triple helix domain of a STOP-1 polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length STOP-1 polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, STOP-1 variant polynucleotides are at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length.

"Percent (%) nucleic acid sequence identity" with respect to STOP-1-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the STOP-1 nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or can be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "STOP-1-DNA", wherein "STOP-1-DNA" represents a hypothetical STOP-1-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "STOP-1-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides. Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

In other embodiments, STOP-1 variant polynucleotides are nucleic acid molecules that encode a STOP-1 polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length STOP-1 polypeptide as disclosed herein. STOP-1 variant polypeptides can be those that are encoded by a STOP-1 variant polynucleotide.

The term "full-length coding region" when used in reference to a nucleic acid encoding a STOP-1 polypeptide refers to the sequence of nucleotides which encode the full-length STOP-1 polypeptide of the invention (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures). The term "full-length coding region" when used in reference to an ATCC deposited nucleic acid refers to the STOP-1 polypeptide-encoding portion of the cDNA that is inserted into the vector deposited with the

ATCC (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures).

"Isolated," when used to describe the various STOP-1 polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and can include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the STOP-1 polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" STOP-1 polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably

linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, can be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42C; or (3) overnight hybridization in a solution that employs 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42C, with a 10 minute wash at 42C in 0.2 x SSC (sodium chloride/sodium citrate) followed by a 10 minute high-stringency wash consisting of 0.1 x SSC containing EDTA at 55C.

"Moderately stringent conditions" can be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately

stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a STOP-1 polypeptide or anti-STOP-1 antibody fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues). Polypeptides and antibodies of this invention that are epitope-tagged are contemplated.

"Biologically active" and "biological activity" and "biological characteristics" with respect to an STOP-1 means (1) having the ability to increase cell proliferation of at least one type of mammalian cell (e.g., 3T3) in vivo or ex vivo; (2) having the ability to specifically bind STOP-1; and/or (3) having the ability to otherwise modulate STOP-1 signaling or STOP-1 activity, except where specified otherwise.

"Biologically active" and "biological activity" and "biological characteristics" with respect to a modified STOP-1 polypeptide or a STOP-1 polypeptide (1) having the ability to partially or fully block, inhibit or neutralize a biological activity of a native STOP-1 (either in an antagonistic or blocking manner); (2) having the ability to specifically bind STOP-1; and/or (3) having the ability to modulate STOP-1 signaling or STOP-1 activity, except where specified otherwise.

"Biologically active" and "biological activity" and "biological characteristics" with respect to an anti-STOP-1 antibody of this invention means (1) having the ability to partially or fully block, inhibit or neutralize a biological activity of a native STOP-1 (either in an antagonistic or blocking manner); (2) having the ability to specifically bind STOP-1; and/or (3) having the ability to modulate STOP-1 signaling or STOP-1 activity, except where specified otherwise. In one preferred embodiment, an antibody of this invention binds to STOP-1 with an affinity of at least 1uM or less, 100nm or less, 50nm or less, 10nm or less, 5nM or less, 1nm or less. As used herein, "antibody variable domain" refers to the portions

of the light and heavy chains of antibody molecules that include amino acid sequences of Complementary Determining Regions (CDRs; ie., CDR1, CDR2, and CDR3), and Framework Regions (FRs). V_H refers to the variable domain of the heavy chain. V_L refers to the variable domain of the light chain. According to the methods used in this invention, the amino acid positions assigned to CDRs and FRs are defined according to Kabat (Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md., 1987 and 1991)). Amino acid numbering of antibodies or antigen binding fragments is also according to that of Kabat.

As used herein, "codon set" refers to a set of different nucleotide triplet sequences used to encode desired variant amino acids. A set of oligonucleotides can be synthesized, for example, by solid phase synthesis, containing sequences that represent all possible combinations of nucleotide triplets provided by the codon set and that will encode the desired group of amino acids. A standard form of codon designation is that of the IUB code, which is known in the art and described herein. A "non-random codon set", as used herein, thus refers to a codon set that encodes select amino acids that fulfill partially, preferably completely, the criteria for amino acid selection as described herein. Synthesis of oligonucleotides with selected nucleotide "degeneracy" at certain positions is known in that art, for example the TRIM approach (Knappek et al.; J. Mol. Biol. (1999), 296:57-86); Garrard & Henner, Gene (1993), 128:103). Such sets of nucleotides having certain codon sets can be synthesized using commercial nucleic acid synthesizers (available from, for example, Applied Biosystems, Foster City, CA), or can be obtained commercially (for example, from Life Technologies, Rockville, MD). Therefore, a set of oligonucleotides synthesized having a particular codon set will typically include a plurality of oligonucleotides with different sequences, the differences established by the codon set within the overall sequence. Oligonucleotides, as used according to the invention, have sequences that allow for hybridization to a variable domain nucleic acid template and also can, but does not necessarily, include restriction enzyme sites useful for, for example, cloning purposes.

"Heterologous DNA" is any DNA that is introduced into a host cell. The DNA can be derived from a variety of sources including genomic DNA, cDNA, synthetic DNA and fusions or combinations of these. The DNA can include DNA from the same cell or cell type as the host or recipient cell or DNA from a different cell type, for example, from a mammal or plant. The DNA can, optionally, include marker or selection genes, for example, antibiotic resistance genes, temperature resistance genes, etc. Host cells encoding heterologous DNAs

comprising the UNQ polypeptides and antibodies of this invention are contemplated as well as their use.

As used herein, "highly diverse position" refers to a position of an amino acid located in the variable regions of the light and heavy chains that have a number of different amino acid represented at the position when the amino acid sequences of known and/or naturally occurring antibodies or antigen binding fragments are compared. The highly diverse positions are typically in the CDR regions. In one aspect, the ability to determine highly diverse positions in known and/or naturally occurring antibodies is facilitated by the data provided by Kabat, Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md., 1987 and 1991). An internet-based database located at http://immuno.bme.nwu.edu provides an extensive collection and alignment of human light and heavy chain sequences and facilitates determination of highly diverse positions in these sequences. According to the invention, an amino acid position is highly diverse if it has preferably from about 2 to about 11, preferably from about 4 to about 9, and preferably from about 5 to about 7 different possible amino acid residue variations at that position. In some embodiments, an amino acid position is highly diverse if it has preferably at least about 2, preferably at least about 4, preferably at least about 6, and preferably at least about 8 different possible amino acid residue variations at that position.

As used herein, “library” refers to a plurality of antibody or antibody fragment sequences (for example, polypeptides of the invention), or the nucleic acids that encode these sequences, the sequences being different in the combination of variant amino acids that are introduced into these sequences according to the methods of the invention.

"Phage display" is a technique by which variant polypeptides are displayed as fusion proteins to a coat protein on the surface of phage, *e.g.*, filamentous phage, particles. A utility of phage display lies in the fact that large libraries of randomized protein variants can be rapidly and efficiently sorted for those sequences that bind to a target molecule with high affinity. Display of peptide and protein libraries on phage has been used for screening millions of polypeptides for ones with specific binding properties. Polyvalent phage display methods have been used for displaying small random peptides and small proteins through fusions to either gene III or gene VIII of filamentous phage. Wells and Lowman, *Curr. Opin. Struct. Biol.*, 3:355-362 (1992), and references cited therein. In monovalent phage display, a protein or peptide library is fused to a gene III or a portion thereof, and expressed at low levels in the presence of wild type gene III protein so that phage particles display one copy or none of the fusion proteins. Avidity effects are reduced relative to polyvalent phage so that

sorting is on the basis of intrinsic ligand affinity, and phagemid vectors are used, which simplify DNA manipulations. Lowman and Wells, *Methods: A companion to Methods in Enzymology,* 3:205-0216 (1991).

A "phagemid" is a plasmid vector having a bacterial origin of replication, *e.g.*, ColE1, and a copy of an intergenic region of a bacteriophage. The phagemid can be used on any known bacteriophage, including filamentous bacteriophage and lambdoid bacteriophage. The plasmid will also generally contain a selectable marker for antibiotic resistance. Segments of DNA cloned into these vectors can be propagated as plasmids. When cells harboring these vectors are provided with all genes necessary for the production of phage particles, the mode of replication of the plasmid changes to rolling circle replication to generate copies of one strand of the plasmid DNA and package phage particles. The phagemid can form infectious or non-infectious phage particles. This term includes phagemids which contain a phage coat protein gene or fragment thereof linked to a heterologous polypeptide gene as a gene fusion such that the heterologous polypeptide is displayed on the surface of the phage particle.

The term "phage vector" means a double stranded replicative form of a bacteriophage containing a heterologous gene and capable of replication. The phage vector has a phage origin of replication allowing phage replication and phage particle formation. The phage is preferably a filamentous bacteriophage, such as an M13, f1, fd, Pf3 phage or a derivative thereof, or a lambdoid phage, such as lambda, 21, phi80, phi81, 82, 424, 434, etc., or a derivative thereof.

As used herein, "target amino acid" refers to an amino acid that belongs to the group of amino acids that are collectively the most commonly occurring amino acids found at a particular position of known and/or natural antibodies or antigen binding fragments. In some embodiments, the most commonly occurring amino acids" are those amino acids that are found in a particular position in preferably at least about 50%, preferably at least about 70%, preferably at least about 80%, preferably at least about 90%, preferably all of sequences of known and/or natural antibodies or antigen binding fragments. In some embodiments, the most commonly occurring amino acids" are those amino acids that are found in a particular position in preferably from about 50% to about 100%, preferably from about 60% to about 90%, preferably from about 70% to about 85%, preferably from about 80% to about 85% of the sequences of known and/or natural antibodies or antigen binding fragments. Known antibodies or antigen biding fragments are those whose sequences are available in the art, such as those available in publicly-accessible databases, such as the database of Kabat ("Sequence of Proteins of Immunological Interest, National Institutes of Health, Bethesda,

Md., 1987 and 1991) and/or as located at http://immuno.bme.nwu.edu. The amino acid position is preferably a position in the CDR region. A target group of amino acids refers to a group of target amino acids for a particular position. Preferably, a target amino acid is not a cysteine residue. For positions in the light chain CDR1, CDR2, CDR3, and for heavy chain CDR1 and CDR2, typically, a target group of amino acids can include from preferably about two to about eleven, preferably from about 4 to about 9, preferably from about 5 to about 7, preferably about 6 amino acids at a particular highly diverse and solvent-accessible position of the source sequence.

The term "proteoglycan" refers to a molecule where at least one glycosaminoglycan side chain is covalently attached to the protein core of the molecule. A proteoglycan synthesis deficient cell line according to this invention includes a cell line that is deficient in galactosyltransferase I. According to one preferred embodiment, the cell line is a CHO-psbg cell line.

The term "antagonist" is any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native STOP-1 polypeptide and that specifically binds to a native STOP-1 polypeptide, wherein the binding of the antagonist (1) is to a native STOP-1 polypeptide in oligomeric form, (2) is to residues 94-243 of native human STOP-1 and/or (3) can be inhibited (e.g., as observed in a competitive ELISA assay using STOP-1 and 6B12) by a monoclonal antibody of this invention (e.g., a deposited antibody of this invention, etc.). According to one embodiment, the antagonist is a polypeptide. According to another embodiment, the 6B12 antibody can inhibit the binding of the antagonist to STOP-1. According to another embodiment, the antagonist binds to a residue within residues 33-52 or 33-53 of human STOP-1 or a non-human STOP-1 equivalent thereof.

The term "small molecule antagonist" refers to any molecule wherein the molecular weight is 1500 daltons or less and is an antagonist according to this invention. According to one embodiment the small molecule antagonist is below about 500 Daltons.

According to one preferred embodiment, the antagonist blocks, inhibits or neutralizes cell proliferation in cells expressing native STOP-1. In one embodiment, the antagonist or small molecule antagonist prevents migration of a cell to which STOP-1 binds. In one preferred embodiment, the antagonist or small molecule antagonist specifically binds to a trimeric form of STOP-1. Suitable antagonists include antibodies, amino acid sequence variants of native STOP-1 polypeptides, peptides, of this invention etc. Methods for identifying antagonists of a STOP-1 polypeptide can comprise contacting a STOP-1

polypeptide with a candidate antagonist molecule and measuring a detectable change in one or more biological activities associated with the STOP-1 polypeptide.

The term "potentiator" refers to any molecule that enhances a biological activity of a native STOP-1 polypeptide and that specifically binds to a native STOP-1 polypeptide, wherein the potentiator can bind to an oligomeric form of a native STOP-1 polypeptide and has at least one additional activity selected from the group consisting of (1) is capable of binding to a residue in residues 94-243 of native human STOP-1, (2) is capable of aggregating STOP-1 on a cell; and (3) can be competed by a monoclonal antibody an S7 or S4 antibody of this invention (e.g., as observed in a competitive ELISA assay using STOP-1, S7 or S4 and the potentiator). According to one embodiment, the potentiator increases the binding of STOP-1 to a cell (e.g., HUVEC cells, HeLa cells, and HT1080 cells). In one preferred embodiment, the agonist binds to a trimeric form of STOP-1. Methods for identifying agonists of a STOP-1 polypeptide can comprise contacting a cell that binds STOP-1 with a STOP-1 polypeptide and the candidate agonist and measuring a detectable change in one or more biological activities associated with the STOP-1 polypeptide (e.g., increased binding of the STOP-1 polypeptide, cell proliferation or cell migration).

"Treating" or "treatment" or "alleviation" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented. These terms indicate the therapeutic and prophylactic uses herein are successful if they ameliorate, lessen or decrease the symptoms, complications or other problems associated with a disease or ameliorate, lessen or decrease the chance of onset or frequency of the symptoms, complications or other problems associated with a disease.

A subject or mammal is successfully "treated" for a STOP-1 polypeptide-expressing cancer if, after receiving a therapeutic amount of an antagonist according to the methods of the present invention, the patient shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of cancer cells or absence of the cancer cells; reduction in the tumor size; inhibition (i.e., slow to some extent and preferably stop) of cancer cell infiltration into peripheral organs including the spread of cancer into soft tissue and bone; inhibition (i.e., slow to some extent and preferably stop) of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief to some extent, one or more of the symptoms associated with the specific cancer; reduced morbidity and mortality, and improvement in quality of life issues. To the extent the anti-STOP-1 antibody or STOP-1

binding oligopeptide can prevent growth and/or kill existing cancer cells, it can be cytostatic and/or cytotoxic. Reduction of these signs or symptoms can also be felt by the patient.

A subject or mammal is successfully "treated" for abnormal angiogenesis if, after receiving a therapeutic amount of an antagonist or agonist according to the methods of the present invention, the patient shows observable and/or measurable [TO BE FILLED IN]; and/or relief to some extent, one or more of the symptoms associated with the abnormal angiogenesis; and improvement in quality of life issues.

The above parameters for assessing successful treatment and improvement in the disease are readily measurable by procedures familiar to a physician. For cancer therapy, efficacy can be measured, for example, by assessing the time to disease progression (TTP) and/or determining the response rate (RR). Metastasis can be determined by staging tests and by bone scan and tests for calcium level and other enzymes to determine spread to the bone. CT scans can also be done to look for spread to the pelvis and lymph nodes in the area. Chest X-rays and measurement of liver enzyme levels by known methods are used to look for metastasis to the lungs and liver, respectively. Other known methods for monitoring the disease include transrectal ultrasonography (TRUS) and transrectal needle biopsy (TRNB).

For bladder cancer, which is a more localized cancer, methods to determine progress of disease include urinary cytologic evaluation by cystoscopy, monitoring for presence of blood in the urine, visualization of the urothelial tract by sonography or an intravenous pyelogram, computed tomography (CT) and magnetic resonance imaging (MRI). The presence of distant metastases can be assessed by CT of the abdomen, chest x-rays, or radionuclide imaging of the skeleton.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of the treatment of, alleviating the symptoms of or diagnosis of a cancer refers to any animal classified as a mammal (aka "patient"), including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and

concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN®, polyethylene glycol (PEG), and PLURONICS®.

By "solid phase" or “solid support” is meant a non-aqueous matrix to which an antibody, an antagonist or a polypeptide of the present invention can adhere or attach. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

As used herein, the term "immunoadhesin" designates antibody-like molecules that combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity that is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand - such as a portion of a native STOP-1 protein. The immunoglobulin constant domain sequence in the immunoadhesin can be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD, or IgM.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a STOP-1 polypeptide, an antibody thereto or a STOP-1 binding oligopeptide) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small" molecule or "small" organic molecule is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide, antibody, antagonist or composition as disclosed herein is an amount sufficient to carry out a specifically stated purpose. An "effective amount" can be determined empirically and by known methods relating to the stated purpose.

The term "therapeutically effective amount" refers to an amount of an antibody, polypeptide or antagonist of this invention effective to "treat" a disease or disorder in a mammal (aka patient). In the case of cancer, the therapeutically effective amount of the drug can reduce the number of cancer cells; reduce the tumor size; inhibit (i.e., slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. See the definition herein of "treating". To the extent the drug can prevent growth and/or kill existing cancer cells, it can be cytostatic and/or cytotoxic.

A "growth inhibitory amount" of a polypeptide, antibody, antagonist or composition of this invention is an amount capable of inhibiting the growth of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "growth inhibitory amount" of a polypeptide, antibody, antagonist or composition of this invention for purposes of inhibiting neoplastic cell growth can be determined empirically and by known methods or by examples provided herein.

A "cytotoxic amount" of a polypeptide, antibody, antagonist or composition of this invention is an amount capable of causing the destruction of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "cytotoxic amount" of a polypeptide, antibody, antagonist or composition of this invention for purposes of inhibiting neoplastic cell growth can be determined empirically and by methods known in the art.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-STOP-1 monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-STOP-1 antibody compositions with polyepitopic specificity, polyclonal antibodies, single chain anti-STOP-1 antibodies, and fragments of anti-STOP-1 antibodies (see below) as long as they specifically bind a native STOP-1 polypeptide and/or exhibit a biological activity or immunological activity of this invention. According to one embodiment, the antibody binds to an oligomeric form of STOP-1, e.g., a trimeric form. In a further embodiment, the antibody specifically binds to human STOP-1 between residues 94-

243. According to another embodiment, the antibody specifically binds to STOP-1, which binding can be inhibited by a monoclonal antibody of this invention (e.g., a deposited antibody of this invention, etc.). The phrase "functional fragment or analog" of an antibody is a compound having a qualitative biological activity in common with an antibody to which it is being referred. For example, a functional fragment or analog of an anti-STOP-1 antibody can be one which can specifically bind to a STOP-1 molecule. In one embodiment, the antibody can prevent or substantially reduce the ability of a STOP-1 molecule to induce cell proliferation. The term "immunoglobulin" (Ig) is used interchangeably with "antibody" herein.According to one embodiment, an antibody of this invention does not bind to a peptide having the amino acid sequence GWNSVSRIIIEELPK.

An "isolated antibody" is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and can include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains (an IgM antibody consists of 5 of the basic heterotetramer unit along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain). In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to a H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ε isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain (C_L) at its other end. The V_L is aligned with the

V_H and the C_L is aligned with the first constant domain of the heavy chain (C_H1). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the different classes of antibodies, see, e.g., Basic and Clinical Immunology, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α, δ, ε, γ, and μ, respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, e.g., humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

The term "variable" refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and define specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable domains. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-12 amino acids long. The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (e.g. around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L, and around about 1-

35 (H1), 50-65 (H2) and 95-102 (H3) in the V_H (in one embodiment, H1 is around about 31-35); Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (*e.g.* residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the V_L, and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the V_H; Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)).

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that can be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations which include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they can be synthesized uncontaminated by other antibodies. The modifier "monoclonal" is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies useful in the present invention can be prepared by the hybridoma methodology first described by Kohler et al., Nature, 256:495 (1975), or can be made using recombinant DNA methods in bacterial, eukaryotic animal or plant cells (see, e.g., U.S. Patent No. 4,816,567). The "monoclonal antibodies" can also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature, 352:624-628 (1991), Marks et al., J. Mol. Biol., 222:581-597 (1991), and the Examples below, for example.

The monoclonal antibodies herein include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit a biological activity of this invention (see U.S. Patent No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (*e.g.* Old World Monkey, Ape etc), and human constant region sequences.

An "intact" antibody is one which comprises an antigen-binding site as well as a C_L and at least heavy chain constant domains, C_H1, C_H2 and C_H3. The constant domains can be native sequence constant domains (*e.g.* human native sequence constant domains) or amino acid sequence variant thereof. Preferably, the intact antibody has one or more effector functions.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (see U.S. Patent No. 5,641,870, Example 2; Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments. The expression "linear antibodies" generally refers to the antibodies described in Zapata et al., Protein Eng., 8(10):1057-1062 (1995). Briefly, these antibodies comprise a pair of tandem Fd segments (VH-CH1-VH-CH1) which, together with complementary light chain polypeptides, form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain (C_H1). Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large $F(ab')_2$ fragment which roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having additional few residues at the carboxy terminus of the C_H1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides. The effector functions of antibodies are determined by sequences in the Fc region, which region is also the part recognized by Fc receptors (FcR) found on certain types of cells.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

"Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994); Borrebaeck 1995, infra.

The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10 residues) between the V_H and V_L domains such that inter-chain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, i.e., fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

"Humanized" forms of non-human (*e.g.*, rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies can comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains,

in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., Nature 321:522-525 (1986); Riechmann et al., Nature 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol. 2:593-596 (1992).

A "species-dependent antibody," e.g., a mammalian anti-human IgE antibody, is an antibody which has a stronger binding affinity for an antigen from a first mammalian species than it has for a homologue of that antigen from a second mammalian species. Normally, the species-dependent antibody "bind specifically" to a human antigen (i.e., has a binding affinity (Kd) value of no more than about 1 x 10^{-7} M, preferably no more than about 1 x 10^{-8} and most preferably no more than about 1 x 10^{-9} M) but has a binding affinity for a homologue of the antigen from a second non-human mammalian species which is at least about 50 fold, or at least about 500 fold, or at least about 1000 fold, weaker than its binding affinity for the human antigen. The species-dependent antibody can be of any of the various types of antibodies as defined above, but preferably is a humanized or human antibody.

A "STOP-1 binding oligopeptide" is an oligopeptide that binds, preferably specifically, to a STOP-1 polypeptide as described herein. STOP-1 binding oligopeptides can be chemically synthesized using known oligopeptide synthesis methodology or can be prepared and purified using recombinant technology. STOP-1 binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a STOP-1 polypeptide as described herein. According to one embodiment, the STOP-1 binding oligopeptide binds to the same or overlapping region that the 6B12 antibody binds. STOP-1 binding oligopeptides can be identified without undue experimentation using known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564;

Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in Synthetic Peptides as Antigens, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

A polypeptide, antibody, antagonist or composition of this invention "which binds" an antigen of interest, e.g. a tumor-associated polypeptide antigen target such as STOP-1, is one that binds the antigen with sufficient affinity such that a polypeptide, antibody, antagonist or composition is useful as a diagnostic and/or therapeutic agent in targeting a cell or tissue expressing the antigen, and does not significantly cross-react with other proteins. In such embodiments, the extent of binding of the polypeptide, antibody, antagonist or composition to a "non-target" protein will be less than about 10% of the binding of the polypeptide, antibody, antagonist or composition to its particular target protein as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA). With regard to the binding of a polypeptide, antibody, antagonist or composition to a target molecule, the term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a Kd for the target of at least about 10^{-4} M, alternatively at least about 10^{-5} M, alternatively at least about 10^{-6} M, alternatively at least about 10^{-7} M, alternatively at least about 10^{-8} M, alternatively at least about 10^{-9} M, alternatively at least about 10^{-10} M, alternatively at least about 10^{-11} M, alternatively at least about 10^{-12} M, or greater. In one embodiment, the term "specific binding" refers to binding where a molecule binds to a particular polypeptide or epitope on a

particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope (e.g., a non-STOP-1 protein). It is understood that an antibody that specifically binds to a human native STOP-1 polypeptide may also bind a non-human native STOP-1 polypeptide.

A polypeptide, antibody, antagonist or composition that "inhibits the growth" of tumor cells expressing a STOP-1 polypeptide or a "growth inhibitory" polypeptide, antibody, antagonist or composition is one which results in measurable growth inhibition of cancer cells expressing or overexpressing the appropriate STOP-1 polypeptide. Preferred growth inhibitory polypeptides, antibodies, antagonists or compositions inhibit growth of STOP-1-expressing tumor cells by greater than 20%, preferably from about 20% to about 50%, and even more preferably, by greater than 50% (e.g., from about 50% to about 100%) as compared to the appropriate control, the control typically being tumor cells not treated with the polypeptide, antibody, antagonist or composition being tested. In one embodiment, growth inhibition can be measured at an antibody concentration of about 0.1 to 30 μg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. Growth inhibition of tumor cells *in vivo* can be determined in various ways such as is described in the Experimental Examples section below. The antibody is growth inhibitory in vivo if administration of the anti-STOP-1 antibody at about 1 μg/kg to about 100 mg/kg body weight results in reduction in tumor size or tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies "arm" the cytotoxic cells and are absolutely required for such killing. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on

hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, Annu. Rev. Immunol. 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an in vitro ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 can be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest can be assessed in vivo, e.g., in a animal model such as that disclosed in Clynes et al. (USA) 95:652-656 (1998).

"Fc receptor" or "FcR" describes a receptor that binds to the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see review M. in Daëron, Annu. Rev. Immunol. 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991); Capel et al., Immunomethods 4:25-34 (1994); and de Haas et al., J. Lab. Clin. Med. 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)).

“Human effector cells” are leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least FcγRIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred. The effector cells can be isolated from a native source, e.g., from blood.

“Complement dependent cytotoxicity” or “CDC” refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement

activation, a CDC assay, e.g., as described in Gazzano-Santoro et al., J. Immunol. Methods 202:163 (1996), can be performed.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer. In one embodiment, the cell proliferative disorder is desmoplasia.

"Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

The term abnormal angiogenesis according to this invention occurs when new blood vessels either grow excessively, insufficiently or inappropriately (e.g., the location, timing or onset of the angiogenesis being undesired from a medical standpoint) in a diseased state or such that it causes a diseased state. "Excessive, inappropriate or uncontrolled angiogenesis" occurs in a diseased state when there is new blood vessel growth that contributes to the worsening of the diseased state, such as in cancer, especially vascularized solid tumors and metastatic tumores (including colon, lung cancer (especially small-cell lung cancer), or prostate cancer), diseases caused by ocular neovascularisation, especially diabetic blindness, retinopathies, primarily diabetic retinopathy or age-induced macular degeneration and rubeosis; psoriasis, haemangioblastoma such as haemangioma; inflammatory renal diseases, such as glomerulonephritis, especially mesangioproliferative glomerulonephritis, haemolytic uremic syndrome, diabetic nephropathy or hypertensive nephrosclerosis; various imflammatory diseases, such as arthritis, especially rheumatoid arthritis, inflammatory bowel

disease, psorsasis, sarcoidosis, arterial arteriosclerosis and diseases occurring after transplants, endometriosis or chronic asthma and more than 70 other conditions. The new blood vessels can feed the diseased tissues, destroy normal tissues, and in the case of cancer, the new vessels can allow tumor cells to escape into the circulation and lodge in other organs (tumor metastases). Insufficient angiogenesis occurs when there is inadequate blood vessels growth that contributes to the worsening of a diseased state, e.g., in diseases such as coronary artery disease, stroke, and delayed wound healing. Further, ulcers, strokes, and heart attacks can result from the absence of angiogenesis that normally required for natural healing. The present invention contemplates treating those patients that are at risk of developing the above-mentioned illnesses.

Other patients that are candidates for receiving the STOP-1 antagonists of this invention have, or are at risk for developing, abnormal proliferation of fibrovascular tissue, acne rosacea, acquired immune deficiency syndrome, artery occlusion, atopic keratitis, bacterial ulcers, Bechets disease, blood borne tumors, carotid obstructive disease, choroidal neovascularization, chronic inflammation, chronic retinal detachment, chronic uveitis, chronic vitritis, contact lens overwear, corneal graft rejection, corneal neovascularization, corneal graft neovascularization, Crohn's disease, Eales disease, epidemic keratoconjunctivitis, fungal ulcers, Herpes simplex infections, Herpes zoster infections, hyperviscosity syndromes, Kaposi's sarcoma, leukemia, lipid degeneration, Lyme's disease, marginal keratolysis, Mooren ulcer, Mycobacteria infections other than leprosy, myopia, ocular neovascular disease, optic pits, Osler-Weber syndrome (Osler-Weber-Rendu, osteoarthritis, Pagets disease, pars planitis, pemphigoid, phylectenulosis, polyarteritis, post-laser complications, protozoan infections, pseudoxanthoma elasticum, pterygium keratitis sicca, radial keratotomy, retinal neovascularization, retinopathy of prematurity, retrolental fibroplasias, sarcoid, scleritis, sickle cell anemia, Sogrens syndrome, solid tumors, Stargarts disease, Steven's Johnson disease, superior limbic keratitis, syphilis, systemic lupus, Terrien's marginal degeneration, toxoplasmosis, trauma, tumors of Ewing sarcoma, tumors of neuroblastoma, tumors of osteosarcoma, tumors of retinoblastoma, tumors of rhabdomyosarcoma, ulcerative colitis, vein occlusion, Vitamin A deficiency and Wegeners sarcoidosis, undesired angiogenesis associated with diabetes, parasitic diseases, abnormal wound healing, hypertrophy following surgery, injury or trauma, inhibition of hair growth, inhibition of ovulation and corpus luteum formation, inhibition of implantation and inhibition of embryo development in the uterus.

Anti-angiogenesis therapies are useful in the general treatment of graft rejection, lung inflammation, nephrotic syndrome, preeclampsia, pericardial effusion, such as that associated with pericarditis, and pleural effusion, diseases and disorders characterized by undesirable vascular permeability, e.g., edema associated with brain tumors, ascites associated with malignancies, Meigs' syndrome, lung inflammation, nephrotic syndrome, pericardial effusion and pleural effusion and the like.

Other angiogenesis-dependent diseases that may be treated with the compositions of this invention include angiofibroma (abnormal blood of vessels which are prone to bleeding), neovascular glaucoma (abnormal growth of blood vessels in the eye), arteriovenous malformations (abnormal communication between arteries and veins), nonunion fractures (fractures that will not heal), atherosclerotic plaques (hardening of the arteries), pyogenic granuloma (common skin lesion composed of blood vessels), scleroderma (a form of connective tissue disease), hemangioma (tumor composed of blood vessels), trachoma (leading cause of blindness in the third world), hemophilic joints, vascular adhesions and hypertrophic scars (abnormal scar formation).

Since blood vessels play an important role in the regulation of bone turnover and growth, potentiators or agonists according to this invention may stimulate or enhance of bone and/or cartilage repair from disease or injury or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes. Bone injuries or diseases to be treated with STOP-1 potentiators or agonists of this invention include periodontal diseases, other tooth-repair processes, osteoporosis and fractures.

A "stromal targeting agent" according to this invention is an agent that substantially recognizes and binds stromal tissue compared to other tissue. Stromal tissue is the connective tissue framework of an organ, gland, or other structure, as distinguished from the tissues performing the special function of the organ or part. Examples of stromal targeting agents include antibodies that specifically bind to FAP, fascin, HSP47, mesothelin and prostate stem antigen.

A polypeptide, antibody, antagonist or composition of this invention which "induces cell death" is one which causes a viable cell to become nonviable. The cell is one which expresses a STOP-1 polypeptide, preferably a cell that overexpresses a STOP-1 polypeptide as compared to a normal cell of the same tissue type. Preferably, the cell is a cancer cell, e.g., a breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, thyroid, pancreatic or bladder cell. Cell death *in vitro* can be determined in the absence of

complement and immune effector cells to distinguish cell death induced by antibody-dependent cell-mediated cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC). Thus, the assay for cell death can be performed using heat inactivated serum (i.e., in the absence of complement) and in the absence of immune effector cells. To determine whether a polypeptide, antibody, antagonist or composition of this invention is able to induce cell death, loss of membrane integrity as evaluated by uptake of propidium iodide (PI), trypan blue (see Moore et al. Cytotechnology 17:1-11 (1995)) or 7AAD can be assessed relative to untreated cells. Preferred cell death-inducing polypeptides, antibodies, antagonists or compositions are those which induce PI uptake in the PI uptake assay in BT474 cells.

A "STOP-1-expressing cell" is a cell which expresses an endogenous or transfected STOP-1 polypeptide either on the cell surface or in a secreted form. A "STOP-1-expressing cancer" is a cancer comprising cells that have a STOP-1 polypeptide present on the cell surface or that produce and secrete a STOP-1 polypeptide. In another embodiment, a "STOP-1-expressing cancer" optionally produces and secretes sufficient levels of STOP-1 polypeptide, such that a polypeptide, antibody, antagonist or composition of this invention can bind thereto and have a therapeutic effect with respect to the cancer. A cancer which "overexpresses" a STOP-1 polypeptide is one which has significantly higher levels of STOP-1 polypeptide at the cell surface thereof, or produces and secretes, compared to a noncancerous cell of the same tissue type. Such overexpression can be caused by gene amplification or by increased transcription or translation. STOP-1 polypeptide overexpression can be determined in a diagnostic or prognostic assay by evaluating increased levels of the STOP-1 protein present on the surface of a cell, or secreted by the cell (e.g., via an immunohistochemistry assay using anti-STOP-1 antibodies prepared against an isolated STOP-1 polypeptide which can be prepared using recombinant DNA technology from an isolated nucleic acid encoding the STOP-1 polypeptide; FACS analysis, etc.). Alternatively, or additionally, one can measure levels of STOP-1 polypeptide-encoding nucleic acid or mRNA in the cell, e.g., via fluorescent *in situ* hybridization using a nucleic acid based probe corresponding to a STOP-1-encoding nucleic acid or the complement thereof; (FISH; see WO98/45479 published October, 1998), Southern blotting, Northern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR). One can also study STOP-1 polypeptide overexpression by measuring shed antigen in a biological fluid such as serum, e.g., using antibody-based assays (see also, e.g., U.S. Patent No. 4,933,294 issued June 12, 1990; WO91/05264 published April 18, 1991; U.S. Patent 5,401,638 issued March 28, 1995; and Sias et al., J. Immunol. Methods 132:73-80 (1990)). Aside from the

above assays, various *in vivo* assays are available to the skilled practitioner. For example, one can expose cells within the body of the mammal to an antibody which is optionally labeled with a detectable label, e.g., a radioactive isotope, and binding of the antibody to cells in the mammal can be evaluated, e.g., by external scanning for radioactivity or by analyzing a biopsy taken from a mammal previously exposed to the antibody.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the polypeptide, antibody, antagonist or composition so as to generate a "labeled" a polypeptide, antibody, antagonist or composition. The label can be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, can catalyze chemical alteration of a substrate compound or composition which is detectable.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32} and radioactive isotopes of Lu), chemotherapeutic agents e.g. methotrexate, adriamicin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A tumoricidal agent causes destruction of tumor cells.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and CYTOXAN® cyclosphosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethiylenethiophosphoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide,

mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimnustine; antibiotics such as the enediyne antibiotics (e. g., calicheamicin, especially calicheamicin gamma1I and calicheamicin omegaI1 (see, e.g., Agnew, Chem Intl. Ed. Engl., 33: 183-186 (1994)); dynemicin, including dynemicin A; bisphosphonates, such as clodronate; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antiobiotic chromophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN® doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti- adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; podophyllinic acid; 2- ethylhydrazide; procarbazine; PSK® polysaccharide complex (JHS Natural Products, Eugene, OR); razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, e.g., TAXOL® paclitaxel (Bristol- Myers Squibb Oncology, Princeton, N.J.), ABRAXANE™ Cremophor-free, albumin-engineered nanoparticle formulation of paclitaxel (American Pharmaceutical Partners, Schaumberg, Illinois), and TAXOTERE® doxetaxel (Rhône-

Poulenc Rorer, Antony, France); chloranbucil; GEMZAR® gemcitabine; 6- thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine; NAVELBINE® vinorelbine; novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluorometlhylornithine (DMFO); retinoids such as retinoic acid; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens and selective estrogen receptor modulators (SERMs), including, for example, tamoxifen (including NOLVADEX® tamoxifen), raloxifene, droloxifene, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and FARESTON· toremifene; aromatase inhibitors that inhibit the enzyme aromatase, which regulates estrogen production in the adrenal glands, such as, for example, 4(5)-imidazoles, aminoglutethimide, MEGASE® megestrol acetate, AROMASIN® exemestane, formestanie, fadrozole, RIVISOR® vorozole, FEMARA® letrozole, and ARIMIDEX® anastrozole; and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; as well as troxacitabine (a 1,3-dioxolane nucleoside cytosine analog); antisense oligonucleotides, particularly those which inhibit expression of genes in signaling pathways implicated in abherant cell proliferation, such as, for example, PKC-alpha, Ralf and H-Ras; ribozymes such as a VEGF expression inhibitor (e.g., ANGIOZYME® ribozyme) and a HER2 expression inhibitor; vaccines such as gene therapy vaccines, for example, ALLOVECTIN® vaccine, LEUVECTIN® vaccine, and VAXID® vaccine; PROLEUKIN® rIL-2; LURTOTECAN® topoisomerase 1 inhibitor; ABARELIX® rmRH; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a STOP-1-expressing cancer cell, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent can be one which significantly reduces the percentage of STOP-1-expressing cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further

information can be found in The Molecular Basis of Cancer, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

"Doxorubicin" is an anthracycline antibiotic. The full chemical name of doxorubicin is (8S-cis)-10-[(3-amino-2,3,6-trideoxy-α-L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione.

The term "package insert" is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, contraindications and/or warnings concerning the use of such therapeutic products.

Table 1

```
/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define      _M     -8      /* value of a match with a stop */

int     _day[26][26] = {
/*      A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0,-2, 0, 0,-4, 1,-1,-1, 0,-1,-2,-1, 0,_M, 1, 0,-2, 1, 1, 0, 0,-6, 0,-3, 0},
/* B */ { 0, 3,-4, 3, 2,-5, 0, 1,-2, 0, 0,-3,-2, 2,_M,-1, 1, 0, 0, 0, 0,-2,-5, 0,-3, 1},
/* C */ {-2,-4,15,-5,-5,-4,-3,-3,-2, 0,-5,-6,-5,-4,_M,-3,-5,-4, 0,-2, 0,-2,-8, 0, 0,-5},
/* D */ { 0, 3,-5, 4, 3,-6, 1, 1,-2, 0, 0,-4,-3, 2,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 2},
/* E */ { 0, 2,-5, 3, 4,-5, 0, 1,-2, 0, 0,-3,-2, 1,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 3},
/* F */ {-4,-5,-4,-6,-5, 9,-5,-2, 1, 0,-5, 2, 0,-4,_M,-5,-5,-4,-3,-3, 0,-1, 0, 0, 7,-5},
```

```
/* G */  { 1, 0,-3, 1, 0,-5, 5,-2,-3, 0,-2,-4,-3, 0,_M,-1,-1,-3, 1, 0, 0,-1,-7, 0,-5, 0},
/* H */  {-1, 1,-3, 1, 1,-2,-2, 6,-2, 0, 0,-2,-2, 2,_M, 0, 3, 2,-1,-1, 0,-2,-3, 0, 0, 2},
/* I */  {-1,-2,-2,-2,-2, 1,-3,-2, 5, 0,-2, 2, 2,-2,_M,-2,-2,-2,-1, 0, 0, 4,-5, 0,-1,-2},
/* J */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */  {-1, 0,-5, 0, 0,-5,-2, 0,-2, 0, 5,-3, 0, 1,_M,-1, 1, 3, 0, 0, 0,-2,-3, 0,-4, 0},
/* L */  {-2,-3,-6,-4,-3, 2,-4,-2, 2, 0,-3, 6, 4,-3,_M,-3,-2,-3,-3,-1, 0, 2,-2, 0,-1,-2},
/* M */  {-1,-2,-5,-3,-2, 0,-3,-2, 2, 0, 0, 4, 6,-2,_M,-2,-1, 0,-2,-1, 0, 2,-4, 0,-2,-1},
/* N */  { 0, 2,-4, 2, 1,-4, 0, 2,-2, 0, 1,-3,-2, 2,_M,-1, 1, 0, 1, 0, 0,-2,-4, 0,-2, 1},
/* O */  {_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,
0,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M},
/* P */  { 1,-1,-3,-1,-1,-5,-1, 0,-2, 0,-1,-3,-2,-1,_M, 6, 0, 0, 1, 0, 0,-1,-6, 0,-5, 0},
/* Q */  { 0, 1,-5, 2, 2,-5,-1, 3,-2, 0, 1,-2,-1, 1,_M, 0, 4, 1,-1,-1, 0,-2,-5, 0,-4, 3},
/* R */  {-2, 0,-4,-1,-1,-4,-3, 2,-2, 0, 3,-3, 0, 0,_M, 0, 1, 6, 0,-1, 0,-2, 2, 0,-4, 0},
/* S */  { 1, 0, 0, 0, 0,-3, 1,-1,-1, 0, 0,-3,-2, 1,_M, 1,-1, 0, 2, 1, 0,-1,-2, 0,-3, 0},
/* T */  { 1, 0,-2, 0, 0,-3, 0,-1, 0, 0, 0,-1,-1, 0,_M, 0,-1,-1, 1, 3, 0, 0,-5, 0,-3, 0},
/* U */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */  { 0,-2,-2,-2,-2,-1,-1,-2, 4, 0,-2, 2, 2,-2,_M,-1,-2,-2,-1, 0, 0, 4,-6, 0,-2,-2},
/* W */  {-6,-5,-8,-7,-7, 0,-7,-3,-5, 0,-3,-2,-4,-4,_M,-6,-5, 2,-2,-5, 0,-6,17, 0, 0,-6},
/* X */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */  {-3,-3, 0,-4,-4, 7,-5, 0,-1, 0,-4,-1,-2,-2,_M,-5,-4,-4,-3,-3, 0,-2, 0, 0,10,-4},
/* Z */  { 0, 1,-5, 2, 3,-5, 0, 2,-2, 0, 0,-2,-1, 1,_M, 0, 3, 0, 0, 0, 0,-2,-6, 0,-4, 4}
};
/*
 */
#include <stdio.h>
#include <ctype.h>

#define    MAXJMP    16      /* max jumps in a diag */
#define    MAXGAP    24      /* don't continue to penalize gaps larger than this */
#define    JMPS      1024    /* max jmps in an path */
#define    MX        4       /* save if there's at least MX-1 bases since last jmp */

#define    DMAT      3       /* value of matching bases */
#define    DMIS      0       /* penalty for mismatched bases */
```

```
#define     DINS0     8     /* penalty for a gap */
#define     DINS1     1     /* penalty per base */
#define     PINS0     8     /* penalty for a gap */
#define     PINS1     4     /* penalty per residue */

struct jmp {
        short               n[MAXJMP];  /* size of jmp (neg for dely) */
        unsigned short      x[MAXJMP];  /* base no. of jmp in seq x */
};                                      /* limits seq to 2^16 -1 */

struct diag {
        int             score;          /* score at last jmp */
        long            offset;         /* offset of prev block */
        short           ijmp;           /* current jmp index */
        struct jmp      jp;             /* list of jmps */
};

struct path {
        int     spc;            /* number of leading spaces */
        short   n[JMPS];        /* size of jmp (gap) */
        int     x[JMPS];        /* loc of jmp (last elem before gap) */
};

char        *ofile;             /* output file name */
char        *namex[2];          /* seq names: getseqs( ) */
char        *prog;              /* prog name for err msgs */
char        *seqx[2];                   /* seqs: getseqs( ) */
int         dmax;               /* best diag: nw( ) */
int         dmax0;              /* final diag */
int         dna;                /* set if dna: main( ) */
int         endgaps;                    /* set if penalizing end gaps */
int         gapx, gapy;         /* total gaps in seqs */
int         len0, len1;         /* seq lens */
int         ngapx, ngapy;       /* total size of gaps */
```

```
int          smax;                  /* max score: nw( ) */
int          *xbm;                  /* bitmap for matching */
long         offset;                /* current offset in jmp file */
struct diag  *dx;                   /* holds diagonals */
struct path  pp[2];                 /* holds path for seqs */

char         *calloc( ), *malloc( ), *index( ), *strcpy( );
char         *getseq( ), *g_calloc( );

/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 *   where file1 and file2 are two dna or two protein sequences.
 *   The sequences can be in upper- or lower-case an may contain ambiguity
 *   Any lines beginning with ';', '>' or '<' are ignored
 *   Max file length is 65535 (limited by unsigned short x in the jmp struct)
 *   A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 *   Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"

static  _dbval[26] = {
        1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static  _pbval[26] = {
        1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
        128, 256, 0xFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
        1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
        1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
```

```
};

main(ac, av)                                                          main
        int     ac;
        char    *av[];
{
        prog = av[0];
        if (ac != 3) {
                fprintf(stderr,"usage: %s file1 file2\n", prog);
                fprintf(stderr,"where file1 and file2 are two dna or two protein sequences.\n");
                fprintf(stderr,"The sequences can be in upper- or lower-case\n");
                fprintf(stderr,"Any lines beginning with ';' or '<' are ignored\n");
                fprintf(stderr,"Output is in the file \"align.out\"\n");
                exit(1);
        }
        namex[0] = av[1];
        namex[1] = av[2];
        seqx[0] = getseq(namex[0], &len0);
        seqx[1] = getseq(namex[1], &len1);
        xbm = (dna)? _dbval : _pbval;

        endgaps = 0;                    /* 1 to penalize endgaps */
        ofile = "align.out";            /* output file */

        nw( );          /* fill in the matrix, get the possible jmps */
        readjmps( );    /* get the actual jmps */
        print( );               /* print stats, alignment */

        cleanup(0);     /* unlink any tmp files */
}
```

/* do the alignment, return best score: main( )

```
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
* a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw( )                                                                  nw
{
        char        *px, *py;           /* seqs and ptrs */
        int         *ndely, *dely; /* keep track of dely */
        int         ndelx, delx;   /* keep track of delx */
        int         *tmp;          /* for swapping row0, row1 */
        int         mis;           /* score for each type */
        int         ins0, ins1;    /* insertion penalties */
        register         id;            /* diagonal index */
        register         ij;            /* jmp index */
        register         *col0, *col1;  /* score for curr, last row */
        register         xx, yy;        /* index into seqs */

        dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

        ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
        dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
        col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
        col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
        ins0 = (dna)? DINS0 : PINS0;
        ins1 = (dna)? DINS1 : PINS1;

        smax = -10000;
        if (endgaps) {
                for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
                        col0[yy] = dely[yy] = col0[yy-1] - ins1;
                        ndely[yy] = yy;
                }
```

```
        col0[0] = 0;    /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
     */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
         */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
                                                            ...nw
        for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
            mis = col0[yy-1];
            if (dna)
                mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
            else
                mis += _day[*px-'A'][*py-'A'];

            /* update penalty for del in x seq;
             * favor new del over ongong del
             * ignore MAXGAP if weighting endgaps
```

```
 */
if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
        } else {
                dely[yy] -= ins1;
                ndely[yy]++;
        }
} else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
        } else
                ndely[yy]++;
}

/* update penalty for del in y seq;
 * favor new del over ongong del
 */
if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
        } else {
                delx -= ins1;
                ndelx++;
        }
} else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
        } else
                ndelx++;
```

```
}

/* pick the maximum score; we're favoring
 * mis over any del and delx over dely
 */
                                                        ...nw
id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
        col1[yy] = mis;
else if (delx >= dely[yy]) {
        col1[yy] = delx;
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                dx[id].ijmp++;
                if (++ij >= MAXJMP) {
                        writejmps(id);
                        ij = dx[id].ijmp = 0;
                        dx[id].offset = offset;
                        offset += sizeof(struct jmp) + sizeof(offset);
                }
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
}
else {
        col1[yy] = dely[yy];
        ij = dx[id].ijmp;
if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                dx[id].ijmp++;
                if (++ij >= MAXJMP) {
                        writejmps(id);
```

```
                    ij = dx[id].ijmp = 0;
                    dx[id].offset = offset;
                    offset += sizeof(struct jmp) + sizeof(offset);
                }
            }
            dx[id].jp.n[ij] = -ndely[yy];
            dx[id].jp.x[ij] = xx;
            dx[id].score = dely[yy];
        }
        if (xx == len0 && yy < len1) {
            /* last col
             */
            if (endgaps)
                col1[yy] -= ins0+ins1*(len1-yy);
            if (col1[yy] > smax) {
                smax = col1[yy];
                dmax = id;
            }
        }
    }
    if (endgaps && xx < len0)
        col1[yy-1] -= ins0+ins1*(len0-xx);
    if (col1[yy-1] > smax) {
        smax = col1[yy-1];
        dmax = id;
    }
    tmp = col0; col0 = col1; col1 = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);              }
/*
 *
```

```
 * print( ) -- only routine visible outside this module
 *
 * static:
 * getmat( ) -- trace back best path, count matches: print( )
 * pr_align( ) -- print alignment of described in array p[]: print( )
 * dumpblock( ) -- dump a block of lines with numbers, stars: pr_align( )
 * nums( ) -- put out a number line: dumpblock( )
 * putline( ) -- put out a line (name, [num], seq, [num]): dumpblock( )
 * stars( ) - -put a line of stars: dumpblock( )
 * stripname( ) -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC   3
#define P_LINE      256     /* maximum output line */
#define P_SPC       3       /* space between name or num and seq */

extern _day[26][26];
int     olen;           /* set output line length */
FILE    *fx;            /* output file */

print( )                                                        print
{
        int     lx, ly, firstgap, lastgap;      /* overlap */

        if ((fx = fopen(ofile, "w")) == 0) {
                fprintf(stderr,"%s: can't write %s\n", prog, ofile);
                cleanup(1);
        }
        fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
        fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
        olen = 60;
        lx = len0;
```

```
	ly = len1;
	firstgap = lastgap = 0;
	if (dmax < len1 - 1) {	/* leading gap in x */
		pp[0].spc = firstgap = len1 - dmax - 1;
		ly -= pp[0].spc;
	}
	else if (dmax > len1 - 1) {	/* leading gap in y */
		pp[1].spc = firstgap = dmax - (len1 - 1);
		lx -= pp[1].spc;
	}
	if (dmax0 < len0 - 1) {	/* trailing gap in x */
		lastgap = len0 - dmax0 -1;
		lx -= lastgap;
	}
	else if (dmax0 > len0 - 1) {	/* trailing gap in y */
		lastgap = dmax0 - (len0 - 1);
		ly -= lastgap;
	}
	getmat(lx, ly, firstgap, lastgap);
	pr_align( );
}
/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)                                    getmat
	int	lx, ly;			/* "core" (minus endgaps) */
	int	firstgap, lastgap;		/* leading trailing overlap */
{
	int		nm, i0, i1, siz0, siz1;
	char		outx[32];
	double		pct;
	register		n0, n1;
	register char	*p0, *p1;
```

```
/* get total matches, score
 */
i0 = i1 = siz0 = siz1 = 0;
p0 = seqx[0] + pp[1].spc;
p1 = seqx[1] + pp[0].spc;
n0 = pp[1].spc + 1;
n1 = pp[0].spc + 1;

nm = 0;
while ( *p0 && *p1 ) {
        if (siz0) {
                p1++;
                n1++;
                siz0--;
        }
        else if (siz1) {
                p0++;
                n0++;
                siz1--;
        }
        else {
                if (xbm[*p0-'A']&xbm[*p1-'A'])
                        nm++;
                if (n0++ == pp[0].x[i0])
                        siz0 = pp[0].n[i0++];
                if (n1++ == pp[1].x[i1])
                        siz1 = pp[1].n[i1++];
                p0++;
                p1++;
        }
}

/* pct homology:
```

```
 * if penalizing endgaps, base is the shorter seq
 * else, knock off overhangs and take shorter core
 */
if (endgaps)
        lx = (len0 < len1)? len0 : len1;
else
        lx = (lx < ly)? lx : ly;
pct = 100.*(double)nm/(double)lx;
fprintf(fx, "\n");
fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);

fprintf(fx, "<gaps in first sequence: %d", gapx);                    ...getmat
if (gapx) {
        (void) sprintf(outx, " (%d %s%s)",
                ngapx, (dna)? "base":"residue", (ngapx == 1)? "":"s");
        fprintf(fx,"%s", outx);

fprintf(fx, ", gaps in second sequence: %d", gapy);
if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
                ngapy, (dna)? "base":"residue", (ngapy == 1)? "":"s");
        fprintf(fx,"%s", outx);
}
if (dna)
        fprintf(fx,
        "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per
base)\n",
        smax, DMAT, DMIS, DINS0, DINS1);
else
        fprintf(fx,
        "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per
residue)\n",
        smax, PINS0, PINS1);
```

```
        if (endgaps)
                fprintf(fx,
                "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
                firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
                lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
        else
                fprintf(fx, "<endgaps not penalized\n");
}

static          nm;             /* matches in core -- for checking */
static          lmax;           /* lengths of stripped file names */
static          ij[2];          /* jmp index for a path */
static          nc[2];          /* number at start of current line */
static          ni[2];          /* current elem number -- for gapping */
static          siz[2];
static char     *ps[2];         /* ptr to current element */
static char     *po[2];         /* ptr to next output char slot */
static char     out[2][P_LINE];         /* output line */
static char     star[P_LINE]; /* set by stars( ) */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align( )                                                             pr_align
{
        int             nn;     /* char count */
        int             more;
        register                i;

        for (i =  0, lmax = 0; i < 2; i++) {
                nn = stripname(namex[i]);
                if (nn > lmax)
                        lmax = nn;
```

```
        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];         }
    for (nn = nm = 0, more = 1; more; ) {
        for (i = more = 0; i < 2; i++) {
            /*
             * do we have more of this sequence?
             */
            if (!*ps[i])
                continue;

            more++;

            if (pp[i].spc) { /* leading space */
                *po[i]++ = ' ';
                pp[i].spc--;
            }
            else if (siz[i]) {      /* in a gap */
                *po[i]++ = '-';
                siz[i]--;
            }
            else {          /* we're putting a seq element
                             */
                *po[i] = *ps[i];
                if (islower(*ps[i]))
                    *ps[i] = toupper(*ps[i]);
                po[i]++;
                ps[i]++;

                /*
                 * are we at next gap for this seq?
```

...pr_align

```
                                */
                                if (ni[i] == pp[i].x[ij[i]]) {
                                        /*
                                         * we need to merge all gaps
                                         * at this location
                                         */
                                        siz[i] = pp[i].n[ij[i]++];
                                        while (ni[i] == pp[i].x[ij[i]])
                                                siz[i] += pp[i].n[ij[i]++];
                                }
                                ni[i]++;
                        }
                }
                if (++nn == olen || !more && nn) {
                        dumpblock( );
                        for (i = 0; i < 2; i++)
                                po[i] = out[i];
                        nn = 0;
                }
        }
}

/*
 * dump a block of lines, including numbers, stars: pr_align( )
 */
static
dumpblock( )                                                    dumpblock
{
        register        i;

        for (i = 0; i < 2; i++)
*po[i]-- = '\0';

                                                                ...dumpblock
        (void) putc('\n', fx);
```

```
        for (i = 0; i < 2; i++) {
                if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
                        if (i == 0)
                                nums(i);
                        if (i == 0 && *out[1])
                                stars( );
                        putline(i);
                        if (i == 0 && *out[1])
                                fprintf(fx, star);
                        if (i == 1)
                                nums(i);
                }
        }
}

/*
 * put out a number line: dumpblock( )
 */
static
nums(ix)                                                                nums
        int     ix;     /* index in out[] holding seq line */
{
        char            nline[P_LINE];
        register                i, j;
        register char   *pn, *px, *py;

        for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
                *pn = ' ';
        for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
                if (*py == ' ' || *py == '-')
                        *pn = ' ';
                else {
                        if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                                j = (i < 0)? -i : i;
```

```
                        for (px = pn; j; j /= 10, px--)
                                *px = j%10 + '0';
                        if (i < 0)
                                *px = '-';
                }
                else
                        *pn = ' ';
                i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
            (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock( )
 */
static
putline(ix)                                                         putline
        int     ix;                     {

                                                                    ...putline
        int             i;
        register char   *px;

        for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
                (void) putc(*px, fx);
        for (; i < lmax+P_SPC; i++)
                (void) putc(' ', fx);

        /* these count from 1:
```

```
        * ni[] is current element (from 1)
        * nc[] is number at start of current line
        */
        for (px = out[ix]; *px; px++)
                (void) putc(*px&0x7F, fx);
        (void) putc('\n', fx);
}


/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock( )
 */
static
stars( )                                                        stars
{
        int             i;
        register char   *p0, *p1, cx, *px;

        if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
           !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
                return;
        px = star;
        for (i = lmax+P_SPC; i; i--)
                *px++ = ' ';

        for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
                if (isalpha(*p0) && isalpha(*p1)) {

                        if (xbm[*p0-'A']&xbm[*p1-'A']) {
                                cx = '*';
                                nm++;
                        }
                        else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                                cx = '.';
```

```
				else
					cx = ' ';
			}
			else
				cx = ' ';
			*px++ = cx;
		}
		*px++ = '\n';
		*px = '\0';
}
/*
 * strip path or prefix from pn, return len: pr_align( )
 */
static
stripname(pn)                                                   stripname
		char	*pn;	/* file name (may be path) */
{
		register char  *px, *py;

		py = 0;
		for (px = pn; *px; px++)
			if (*px == '/')
				py = px + 1;
		if (py)
			(void) strcpy(pn, py);
		return(strlen(pn));

}


/*
 * cleanup( ) -- cleanup any tmp file
 * getseq( ) -- read in seq, set dna, len, maxlen
 * g_calloc( ) -- calloc( ) with error checkin
```

```
 * readjmps( ) -- get the good jmps, from tmp file if necessary
 * writejmps( ) -- write a filled array of jmps to a tmp file: nw( )
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";         /* tmp file for jmps */
FILE    *fj;

int     cleanup( );                         /* cleanup tmp file */
long    lseek( );

/*
 * remove any tmp file if we blow
 */
cleanup(i)                                                          cleanup
        int     i;
{
        if (fj)
                (void) unlink(jname);
        exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
getseq(file, len)                                                   getseq
        char    *file;  /* file name */
        int     *len;   /* seq len */
{
        char            line[1024], *pseq;
```

```
register char  *px, *py;
int            natgc, tlen;
FILE           *fp;

if ((fp = fopen(file,"r")) == 0) {
        fprintf(stderr,"%s: can't read %s\n", prog, file);
        exit(1);
}
tlen = natgc = 0;
while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
                continue;
        for (px = line; *px != '\n'; px++)
                if (isupper(*px) || islower(*px))
                        tlen++;
}
if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr,"%s: malloc( ) failed to get %d bytes for %s\n", prog, tlen+6,
file);
        exit(1);
}
pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
```

...getseq

```
py = pseq + 4;
*len = tlen;
rewind(fp);

while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
                continue;
        for (px = line; *px != '\n'; px++) {
                if (isupper(*px))
                        *py++ = *px;
```

```
                else if (islower(*px))
                        *py++ = toupper(*px);
                if (index("ATGCU",*(py-1)))
                        natgc++;
            }
        }
        *py++ = '\0';
        *py = '\0';
        (void) fclose(fp);
        dna = natgc > (tlen/3);
        return(pseq+4);
}

char    *
g_calloc(msg, nx, sz)                                                    g_calloc
        char    *msg;           /* program, calling routine */
        int     nx, sz;         /* number and size of elements */
{
        char            *px, *calloc( );

        if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
                if (*msg) {
                        fprintf(stderr, "%s: g_calloc( ) failed %s (n=%d, sz=%d)\n", prog, msg,
nx, sz);
                        exit(1);
                }
        }
        return(px);
}

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main( )
 */
readjmps( )                                                              readjmps
```

```
{
        int             fd = -1;
        int             siz, i0, i1;
        register        i, j, xx;

        if (fj) {
                (void) fclose(fj);
                if ((fd = open(jname, O_RDONLY, 0)) < 0) {
                        fprintf(stderr, "%s: can't open( ) %s\n", prog, jname);
                        cleanup(1);
                }
        }
        for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
                while (1) {
                        for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                                ;
                                                                        ...readjmps
                        if (j < 0 && dx[dmax].offset && fj) {
                                (void) lseek(fd, dx[dmax].offset, 0);
                                (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
                                (void) read(fd, (char *)&dx[dmax].offset,
sizeof(dx[dmax].offset));
                                dx[dmax].ijmp = MAXJMP-1;
                        }
                        else
                                break;
                }
                if (i >= JMPS) {
                        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
                        cleanup(1);
                }
                if (j >= 0) {
                        siz = dx[dmax].jp.n[j];
                        xx = dx[dmax].jp.x[j];
```

```
                        dmax += siz;
                        if (siz < 0) {          /* gap in second seq */
                                pp[1].n[i1] = -siz;
                                xx += siz;
                                /* id = xx - yy + len1 - 1
                                 */
                                pp[1].x[i1] = xx - dmax + len1 - 1;
                                gapy++;
                                ngapy -= siz;
/* ignore MAXGAP when doing endgaps */
                                siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
                                i1++;
                        }
                        else if (siz > 0) {     /* gap in first seq */
                                pp[0].n[i0] = siz;
                                pp[0].x[i0] = xx;
                                gapx++;
                                ngapx += siz;
/* ignore MAXGAP when doing endgaps */
                                siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
                                i0++;
                        }
                }
                else
                        break;
        }

        /* reverse the order of jmps
         */
        for (j = 0, i0--; j < i0; j++, i0--) {
                i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
                i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
        }
        for (j = 0, i1--; j < i1; j++, i1--) {
```

```
                i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
                i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
        }
        if (fd >= 0)
                (void) close(fd);
        if (fj) {
                (void) unlink(jname);
                fj = 0;
                offset = 0;     }                       }

/*
 * write a filled jmp struct offset of the prev one (if any): nw( )
 */
writejmps(ix)                                                   writejmps
        int     ix;
{
        char    *mktemp( );

        if (!fj) {
                if (mktemp(jname) < 0) {
                        fprintf(stderr, "%s: can't mktemp( ) %s\n", prog, jname);
                        cleanup(1);
                }
                if ((fj = fopen(jname, "w")) == 0) {
                        fprintf(stderr, "%s: can't write %s\n", prog, jname);
                        exit(1);
                }
        }
        (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
```

Table 2

STOP-1	XXXXXXXXXXXXXXX	(Length = 15 amino acids)

Comparison Protein	XXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the STOP-1 polypeptide) =

5 divided by 15 = 33.3%

Table 3

STOP-1	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the STOP-1 polypeptide) =

5 divided by 10 = 50%

Table 4

STOP-1-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

Table 5

STOP-1-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

4 divided by 12 = 33.3%

Compositions and Methods of the Invention

STOP-1 Polypeptide Variants

In addition to the full-length native sequence STOP-1 polypeptides described herein, it is contemplated that STOP-1 polypeptide variants can be prepared. STOP-1 polypeptide variants can be prepared by introducing appropriate nucleotide changes into the STOP-1 DNA, and/or by synthesis of the desired STOP-1 polypeptide. Those skilled in the art will appreciate that amino acid changes can alter post-translational processes of the STOP-1 polypeptide such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence STOP-1 polypeptide or in various domains of the STOP-1 polypeptide described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations can be a substitution, deletion or insertion of one or more codons encoding the STOP-1 polypeptide that results in a change in the amino acid sequence of the STOP-1 polypeptide as compared with the native sequence STOP-1 polypeptide. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the STOP-1 polypeptide. Guidance in determining which amino acid residue can be inserted, substituted or deleted without adversely affecting the desired activity can be found by comparing the sequence of the STOP-1 polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, *i.e.*, conservative amino acid replacements. Insertions or deletions can optionally be in the range of about 1 to 5 amino acids. The variation allowed can be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the STOP-1 polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;
(2) neutral hydrophilic: cys, ser, thr;
(3) acidic: asp, glu;
(4) basic: asn, gln, his, lys, arg;
(5) residues that influence chain orientation: gly, pro; and
(6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also can be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter *et al.*, Nucl. Acids Res., 13:4331 (1986); Zoller *et al.*, Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells *et al.*, Gene, 34:315 (1985)], restriction selection mutagenesis [Wells *et al.*, Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the STOP-1 variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

Modifications of STOP-1 polypeptides

Covalent modifications of STOP-1 polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a STOP-1 polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the STOP-1 polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking the STOP-1 polypeptide to a water-insoluble support matrix or surface for use in the method for purifying anti-STOP-1 antibodies, and vice-versa. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the STOP-1 polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in the native sequence STOP-1 polypeptide (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence STOP-1 polypeptide. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the STOP-1 polypeptide can be accomplished by altering the amino acid sequence. The alteration can be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence STOP-1 polypeptide (for O-linked glycosylation sites). The STOP-1 amino acid sequence can optionally be altered through changes at the DNA level, particularly by mutating the DNA

encoding the STOP-1 polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the STOP-1 polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, *e.g.*, in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the STOP-1 polypeptide can be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, Arch. Biochem. Biophys., 259:52 (1987) and by Edge *et al.*, Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of the STOP-1 polypeptide comprises linking the STOP-1 polypeptide to one of a variety of nonproteinaceous polymers, *e.g.*, polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The STOP-1 polypeptide of the present invention can also be modified in a way to form a chimeric molecule comprising the STOP-1 polypeptide fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the STOP-1 polypeptide with a protein transduction domain which targets the STOP-1 polypeptide for delivery to various tissues and more particularly across the brain blood barrier, using, for example, the protein transduction domain of human immunodeficiency virus TAT protein (Schwarze *et al.,* 1999, Science 285: 1569-72).

In another embodiment, such a chimeric molecule comprises a fusion of the STOP-1 polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the STOP-1 polypeptide. The presence of such epitope-tagged forms of the STOP-1 polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the STOP-1 polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are known in the art. Examples

include poly-histidine (poly-His) or poly-histidine-glycine (poly-His-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field *et al.*, Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan *et al.*, Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky *et al.*, Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp *et al.*, BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin *et al.*, Science, 255:192-194 (1992)]; an α-tubulin epitope peptide [Skinner *et al.*, J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth *et al.*, Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule can comprise a fusion of the STOP-1 polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. Ig fusions of this invention include polypeptides that comprise approximately or only residues 94-243, residues 33-53 or residues 33-52 of human STOP-1 in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions *see* also, U.S. Patent No. 5,428,130 issued June 27, 1995.

Preparation of the STOP-1 polypeptide

The description below relates primarily to production of STOP-1 polypeptides by culturing cells transformed or transfected with a vector containing nucleic acid encoding STOP-1 polypeptides. It is, of course, contemplated that alternative methods that are known in the art can be employed to prepare the STOP-1 polypeptide. For instance, the STOP-1 polypeptide sequence, or portions thereof, can be produced by direct peptide synthesis using solid-phase techniques. *See*, *e.g.*, Stewart *et al.*, Solid-Phase Peptide Synthesis (W.H. Freeman Co.: San Francisco, CA, 1969); Merrifield, J. Am. Chem. Soc., 85: 2149-2154 (1963). *In vitro* protein synthesis can be performed using manual techniques or by automation. Automated synthesis can be accomplished, for instance, with an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the STOP-1 polypeptide can be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length STOP-1 polypeptide.

Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for STOP-1 polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH, and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: A Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook *et al.*, *supra.*

Methods of transfection are known to the ordinarily skilled artisan, for example, $CaPO_4$ treatment and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook *et al.*, *supra*, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw *et al.*, Gene, 23: 315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen *et al.*, J. Bact., 130: 946 (1977) and Hsiao *et al.*, Proc. Natl. Acad. Sci. (USA), 76: 3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, *e.g.*, polybrene or polyornithine, can also be used. For various techniques for transforming mammalian cells, *see*, Keown *et al.*, Methods in Enzymology, 185: 527-537 (1990) and Mansour *et al.*, Nature, 336: 348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include, but are not limited to, eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325); and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, *e.g.*, *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, *e.g.*, *Salmonella typhimurium*, *Serratia*, *e.g.*, *Serratia marcescans*, and

Shigella, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (*e.g.*, *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 can be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA* ; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan*^{r}; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan*^{r}; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, *e.g.*, PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for vectors encoding the STOP-1 polypeptide. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer *et al.*, Bio/Technology, 9: 968-975 (1991)) such as, *e.g.*, *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt *et al.*, J. Bacteriol., 737 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilarum* (ATCC 36,906; Van den Berg *et al.*, Bio/Technology, 8: 135 (1990)), *K. thermotolerans*, and *K. marxianus; yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna *et al.*, J. Basic Microbiol., 28: 265-278 [1988]); *Candida; Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case *et al.*, Proc. Natl. Acad. Sci. USA, 76: 5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, *e.g.*, *Neurospora, Penicillium, Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance *et al.*, Biochem. Biophys. Res. Commun., 112: 284-289 [1983]; Tilburn *et al.*, Gene, 26: 205-221 [1983]; Yelton *et al.*, Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4: 475-479 [1985]). Methylotropic yeasts are suitable herein

and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula, Candida, Kloeckera, Pichia, Saccharomyces, Torulopsis,* and *Rhodotorula.* A list of specific species that are exemplary of this class of yeasts can be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of nucleic acid encoding glycosylated STOP-1 polypeptides are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, J. Gen. Virol., 36: 59 (1977)) ; Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)) ; mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

Selection and Use of a Replicable Vector

The nucleic acid (*e.g.*, cDNA or genomic DNA) encoding a polypeptide or antibody of this invention can be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector can, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence can be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence if the sequence is to be secreted, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques that are known to the skilled artisan.

The polypeptide or antibody of this invention can be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which can be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence can be a component of the vector, or it can be a part of the DNA encoding the polypeptide or antibody that is inserted

into the vector. The signal sequence can be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence can be, *e.g.*, the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences can be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV, or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the nucleic acid encoding the polypeptide or antibody such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4216 (1980). A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7. Stinchcomb *et al.*, Nature, 282: 39 (1979); Kingsman *et al.*, Gene, 7: 141 (1979); Tschemper *et al.*, Gene, 10: 157 (1980). The *trp*1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1. Jones, Genetics, 85: 12 (1977).

Expression and cloning vectors usually contain a promoter operably linked to the nucleic acid sequence encoding the polypeptide or antibody of this invention to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems

(Chang *et al.*, Nature, 275: 615 (1978); Goeddel *et al.*, Nature, 281: 544 (1979)), alkaline phosphatase, a tryptophan (trp) promoter system (Goeddel, Nucleic Acids Res., 8: 4057 (1980); EP 36,776), and hybrid promoters such as the tac promoter (deBoer *et al.*, Proc. Natl. Acad. Sci. USA, 80: 21-25 (1983)). Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the polypeptide or antibody of this invention.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (Hitzeman *et al.*, J. Biol. Chem., 255: 2073 (1980)) or other glycolytic enzymes (Hess *et al.*, J. Adv. Enzyme Reg., 7: 149 (1968); Holland, Biochemistry, 17: 4900 (1978)), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters that are inducible promoters having the additional advantage of transcription controlled by growth conditions are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

Nucleic acid transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus, and Simian Virus 40 (SV40); by heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter; and by heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding a polypeptide or antibody of this invention by higher eukaryotes can be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus

enhancers. The enhancer can be spliced into the vector at a position 5' or 3' to the sequence coding for a polypeptide or antibody of this invention, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding polypeptide or antibody.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of the polypeptide or antibody of this invention in recombinant vertebrate cell culture are described in Gething *et al.*, Nature, 293: 620-625 (1981); Mantei *et al.*, Nature, 281: 40-46 (1979); EP 117,060; and EP 117,058.

Detecting Gene Amplification/Expression

Gene amplification and/or expression can be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA (Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies can be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn can be labeled and the assay can be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, can be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids can be either monoclonal or polyclonal, and can be prepared in any mammal or can be synthesized (e.g., the monoclonal antibodies of this invention). Conveniently, the antibodies can be prepared against a native-sequence STOP-1 polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to DNA encoding the STOP-1 polypeptide and encoding a specific antibody epitope.

Purification of STOP-1 polypeptides

Forms of STOP-1 polypeptides can be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (*e.g.*, TRITON-X™ 100) or by enzymatic cleavage. Cells employed in expression of nucleic acid encoding the STOP-1 polypeptide can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell-lysing agents. According to one embodiment, it is desireabel that the STOP-1 polypeptide is purified from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the STOP-1 polypeptide. Various methods of protein purification can be employed and such methods are known in the art and described, for example, in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice (Springer-Verlag: New York, 1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular STOP-1 polypeptide produced. According to one embodiment, the STOP-1 polypeptides are purified by affinity chromatography using an antibody of this invention.

Assaying inhibition of cell proliferation

The inhibitory activity of antagonists of this invention can be measured using the assays of Examples 13-14 below and other assays known in the art.

Animal models of tumors and cancers (*e.g.*, breast cancer, colon cancer, prostate cancer, lung cancer, etc.) include both non-recombinant and recombinant (transgenic) animals. Non-recombinant animal models include, for example, rodent, *e.g.*, murine models. Such models can be generated by introducing tumor cells into syngeneic mice using standard techniques, *e.g.*, subcutaneous injection, tail vein injection, spleen implantation, intraperitoneal implantation, implantation under the renal capsule, or orthopin implantation, *e.g.*, colon cancer cells implanted in colonic tissue. *See*, *e.g.*, PCT publication No. WO 97/33551, published September 18, 1997. Probably the most often used animal species in oncological studies are immunodeficient mice and, in particular, nude mice. The observation

that the nude mouse with thymic hypo/aplasia could successfully act as a host for human tumor xenografts has lead to its widespread use for this purpose. The autosomal recessive *nu* gene has been introduced into a very large number of distinct congenic strains of nude mouse, including, for example, ASW, A/He, AKR, BALB/c, B10.LP, C17, C3H, C57BL, C57, CBA, DBA, DDD, I/st, NC, NFR, NFS, NFS/N, NZB, NZC, NZW, P, RIII, and SJL. In addition, a wide variety of other animals with inherited immunological defects other than the nude mouse have been bred and used as recipients of tumor xenografts. For further details *see*, *e.g.*, The Nude Mouse in Oncology Research, E. Boven and B. Winograd, eds. (CRC Press, Inc., 1991).

The cells introduced into such animals can be derived from known tumor/cancer cell lines, such as any of the above-listed tumor cell lines, and, for example, the B104-1-1 cell line (stable NIH-3T3 cell line transfected with the *neu* protooncogene); *ras*-transfected NIH-3T3 cells; Caco-2 (ATCC HTB-37); or a moderately well-differentiated grade II human colon adenocarcinoma cell line, HT-29 (ATCC HTB-38); or from tumors and cancers. Samples of tumor or cancer cells can be obtained from patients undergoing surgery, using standard conditions involving freezing and storing in liquid nitrogen. Karmali *et al.*, Br. J. Cancer, 48: 689-696 (1983).

Tumor cells can be introduced into animals such as nude mice by a variety of procedures. The subcutaneous (s.c.) space in mice is very suitable for tumor implantation. Tumors can be transplanted s.c. as solid blocks, as needle biopsies by use of a trochar, or as cell suspensions. For solid-block or trochar implantation, tumor tissue fragments of suitable size are introduced into the s.c. space. Cell suspensions are freshly prepared from primary tumors or stable tumor cell lines, and injected subcutaneously. Tumor cells can also be injected as subdermal implants. In this location, the inoculum is deposited between the lower part of the dermal connective tissue and the s.c. tissue.

Animal models of breast cancer can be generated, for example, by implanting rat neuroblastoma cells (from which the *neu* oncogene was initially isolated), or *neu*-transformed NIH-3T3 cells into nude mice, essentially as described by Drebin *et al.* Proc. Nat. Acad. Sci. USA, 83: 9129-9133 (1986).

Similarly, animal models of colon cancer can be generated by passaging colon cancer cells in animals, *e.g.*, nude mice, leading to the appearance of tumors in these animals. An orthotopic transplant model of human colon cancer in nude mice has been described, for example, by Wang *et al.*, Cancer Research, 54: 4726-4728 (1994) and Too *et al.*, Cancer

Research, 55: 681-684 (1995). This model is based on the so-called "METAMOUSE™" sold by AntiCancer, Inc., (San Diego, California).

Tumors that arise in animals can be removed and cultured *in vitro*. Cells from the *in vitro* cultures can then be passaged to animals. Such tumors can serve as targets for further testing or drug screening. Alternatively, the tumors resulting from the passage can be isolated and RNA from pre-passage cells and cells isolated after one or more rounds of passage analyzed for differential expression of genes of interest. Such passaging techniques can be performed with any known tumor or cancer cell lines.

For example, Meth A, CMS4, CMS5, CMS21, and WEHI-164 are chemically induced fibrosarcomas of BALB/c female mice (DeLeo *et al.*, J. Exp. Med., 146: 720 (1977)), which provide a highly controllable model system for studying the anti-tumor activities of various agents. Palladino *et al.*, J. Immunol., 138: 4023-4032 (1987). Briefly, tumor cells are propagated *in vitro* in cell culture. Prior to injection into the animals, the cell lines are washed and suspended in buffer, at a cell density of about $10x10^6$ to $10x10^7$ cells/ml. The animals are then infected subcutaneously with 10 to 100 ul of the cell suspension, allowing one to three weeks for a tumor to appear.

In addition, the Lewis lung (3LL) carcinoma of mice, which is one of the most thoroughly studied experimental tumors, can be used as an investigational tumor model. Efficacy in this tumor model has been correlated with beneficial effects in the treatment of human patients diagnosed with small-cell carcinoma of the lung (SCCL). This tumor can be introduced in normal mice upon injection of tumor fragments from an affected mouse or of cells maintained in culture. Zupi *et al.*, Br. J. Cancer, 41: suppl. 4, 30 (1980). Evidence indicates that tumors can be started from injection of even a single cell and that a very high proportion of infected tumor cells survive. For further information about this tumor model *see*, Zacharski, Haemostasis, 16: 300-320 (1986).

One way of evaluating the efficacy of a test compound in an animal model with an implanted tumor is to measure the size of the tumor before and after treatment. Traditionally, the size of implanted tumors has been measured with a slide caliper in two or three dimensions. The measure limited to two dimensions does not accurately reflect the size of the tumor; therefore, it is usually converted into the corresponding volume by using a mathematical formula. However, the measurement of tumor size is very inaccurate. The therapeutic effects of a drug candidate can be better described as treatment-induced growth delay and specific growth delay. Another important variable in the description of tumor growth is the tumor volume doubling time. Computer programs for the calculation and

description of tumor growth are also available, such as the program reported by Rygaard and Spang-Thomsen, Proc. 6th Int. Workshop on Immune-Deficient Animals, Wu and Sheng eds. (Basel, 1989), p. 301. It is noted, however, that necrosis and inflammatory responses following treatment can actually result in an increase in tumor size, at least initially. Therefore, these changes need to be carefully monitored, by a combination of a morphometric method and flow cytometric analysis.

Further, recombinant (transgenic) animal models can be engineered by introducing the coding portion of the STOP-1 gene identified herein into the genome of animals of interest, using standard techniques for producing transgenic animals. Animals that can serve as a target for transgenic manipulation include, without limitation, mice, rats, rabbits, guinea pigs, sheep, goats, pigs, and non-human primates, *e.g.*, baboons, chimpanzees and monkeys. Techniques known in the art to introduce a transgene into such animals include pronucleic microinjection (U.S. Patent No. 4,873,191); retrovirus-mediated gene transfer into germ lines (*e.g.*, Van der Putten *et al.*, Proc. Natl. Acad. Sci. USA, 82: 6148-615 (1985)); gene targeting in embryonic stem cells (Thompson *et al.*, Cell, 56: 313-321 (1989)); electroporation of embryos (Lo, Mol. Cell. Biol., 3: 1803-1814 (1983)); and sperm-mediated gene transfer. Lavitrano *et al.*, Cell, 57: 717-73 (1989). For a review, *see* for example, U.S. Patent No. 4,736,866.

For the purpose of the present invention, transgenic animals include those that carry the transgene only in part of their cells ("mosaic animals"). The transgene can be integrated either as a single transgene, or in concatamers, *e.g.*, head-to-head or head-to-tail tandems. Selective introduction of a transgene into a particular cell type is also possible by following, for example, the technique of Lasko *et al.*, Proc. Natl. Acad. Sci. USA, 89: 6232-636 (1992). The expression of the transgene in transgenic animals can be monitored by standard techniques. For example, Southern blot analysis or PCR amplification can be used to verify the integration of the transgene. The level of mRNA expression can then be analyzed using techniques such as *in situ* hybridization, Northern blot analysis, PCR, or immunocytochemistry. The animals are further examined for signs of tumor or cancer development.

Alternatively, "knock-out" animals can be constructed that have a defective or altered gene encoding a STOP-1 polypeptide identified herein, as a result of homologous recombination between the endogenous gene encoding the STOP-1 polypeptide and altered genomic DNA encoding the same polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a particular STOP-1 polypeptide can be used to clone

genomic DNA encoding that polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a particular STOP-1 polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker that can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector. *See, e.g.*, Thomas and Capecchi, Cell, 51: 503 (1987) for a description of homologous recombination vectors. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected. *See, e.g.*, Li *et al.*, Cell, 69: 915 (1992). The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse or rat) to form aggregation chimeras. *See, e.g.*, Bradley, in Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E. J. Robertson, ed. (IRL: Oxford, 1987), pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock-out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized, for instance, by their ability to defend against certain pathological conditions and by their development of pathological conditions due to absence of the STOP-1 polypeptide.

The efficacy of antibodies specifically binding the STOP-1 polypeptides identified herein, and other drug candidates, can be tested also in the treatment of spontaneous animal tumors. A suitable target for such studies is the feline oral squamous cell carcinoma (SCC). Feline oral SCC is a highly invasive, malignant tumor that is the most common oral malignancy of cats, accounting for over 60% of the oral tumors reported in this species. It rarely metastasizes to distant sites, although this low incidence of metastasis can merely be a reflection of the short survival times for cats with this tumor. These tumors are usually not amenable to surgery, primarily because of the anatomy of the feline oral cavity. At present, there is no effective treatment for this tumor. Prior to entry into the study, each cat undergoes complete clinical examination and biopsy, and is scanned by computed tomography (CT). Cats diagnosed with sublingual oral squamous cell tumors are excluded from the study. The tongue can become paralyzed as a result of such tumor, and even if the treatment kills the tumor, the animals may not be able to feed themselves. Each cat is treated repeatedly, over a longer period of time. Photographs of the tumors will be taken daily during the treatment period, and at each subsequent recheck. After treatment, each cat undergoes another CT scan. CT scans and thoracic radiograms are evaluated every 8 weeks thereafter. The data are

evaluated for differences in survival, response, and toxicity as compared to control groups. Positive response may require evidence of tumor regression, preferably with improvement of quality of life and/or increased life span.

In addition, other spontaneous animal tumors, such as fibrosarcoma, adenocarcinoma, lymphoma, chondroma, or leiomyosarcoma of dogs, cats, and baboons can also be tested. Of these, mammary adenocarcinoma in dogs and cats is a preferred model as its appearance and behavior are very similar to those in humans. However, the use of this model is limited by the rare occurrence of this type of tumor in animals.

Assays for Evaluating Angiogenic or Vasculogenic Activity

Assays that are useful for measuring the pro-angiogenic, antiangiogenic, pro-vasculogenic or anti-vasculogenic activity of the agonists, progenitors, antagonists of this invention include the assays of Examples 14 and 26 or other suitable assays known in the art such as those included below.

Assays for wound-healing activity include, for example, those described in Winter, Epidermal Wound Healing, Maibach, HI and Rovee, DT, eds. (Year Book Medical Publishers, Inc., Chicago), pp. 71-112, as modified by the article of Eaglstein and Mertz, J. Invest. Dermatol., 71: 382-384 (1978).

Assays for endothelial cell proliferation include, for example, those described in WO 02/00690 or United States Patent Publication No. 20010036955A1.

Assays for evaluating inhibition of angiogenesis include, for example, the assay described in United States Patent Publication No. 20010036955A1.

Assays for measuring inhibition of endothelial tube formation include, for example, the assay described in United States Patent Publication No. 20010036955A1.

Antibody Binding Studies

Antibody binding studies can be carried out using known assay methods, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. Zola, Monoclonal Antibodies: A Manual of Techniques (CRC Press, Inc., 1987), pp.147-158.

Competitive binding assays rely on the ability of a labeled standard to compete with the test sample analyte for binding with a limited amount of antibody. The amount of target protein in the test sample is inversely proportional to the amount of standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes

bound, the antibodies preferably are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies can conveniently be separated from the standard and analyte that remain unbound.

Sandwich assays involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected. In a sandwich assay, the test sample analyte is bound by a first antibody that is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three-part complex. *See, e.g.*, U.S. Pat. No. 4,376,110. The second antibody can itself be labeled with a detectable moiety (direct sandwich assays) or can be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assay). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

Competitive ELISA assays can be performed to screen polypeptides, antibodies or antagonists for those that specifically bind to STOP-1, which binding can be inhibited by a monoclonal antibody of this invention.

In one example, a competitive ELISA assay can be conducted following the methods described in the Examples (e.g., Example 22). A full length or short form of native STOP-1 protein (2ug/ml in PBS) can be coated on a microtiter plate at 4°C overnight or at room temperature for 2 hours. The wells can be blocked by adding 65ul 1% BSA for 30 minutes followed by 40ul 1% Tween20 for another 30 minutes. Next, the wells can be washed with PBS - 0.05% Tween20 5 times. Various concentrations of S7, S16, S4, F15 or S9 antibody (in ELISA buffer) can be incubated in the wells for 30 minutes at room temperature. Then, polypeptides or antibodies to be tested can be added to different wells for 10 minutes at a concentration that would normally produce 90% binding capacity in the absence of the S7, S16, S4, F15 or S9 antibody. Next, the wells can be washed with PBS - 0.05% Tween20 5 times. Binding can be quantified by methods known in the art.

For immunohistochemistry, the tissue sample can be fresh or frozen or can be embedded in paraffin and fixed with a preservative such as formalin, for example.

Cell-Based Tumor Assays

Cell-based assays and animal models for proliferative disorders, such as tumors, can be used to verify the inhibitory activity of the antagonists of this invention. Useful cell-based assays, animal models and methods include, for example, those set forth in the Examples below.

For example, cells of a cell type known to be involved in a proliferative disorder are transfected with STOP-1 cDNAs herein, and the ability of these cDNAs to induce excessive growth or inhibit growth is analyzed in the presence or absence of an antagonist. If the proliferative disorder is cancer, suitable tumor cells include, for example, stable tumor cell lines such as the B104-1-1 cell line (stable NIH-3T3 cell line transfected with the *neu* protooncogene) and *ras*-transfected NIH-3T3 cells, which can be transfected with the a STOP-1 sequence and monitored for tumorigenic growth. Such transfected cell lines can then be used to test the ability of poly- or monoclonal antibodies or antibody compositions to inhibit tumorigenic cell growth by exerting cytostatic or cytotoxic activity on the growth of the transformed cells, or by mediating antibody-dependent cellular cytotoxicity (ADCC).

In addition, primary cultures derived from tumors in transgenic animals (as described above) can be used in the cell-based assays herein, although stable cell lines are preferred. Techniques to derive continuous cell lines from transgenic animals are known in the art. *See, e.g.*, Small *et al.*, Mol. Cell. Biol., 5: 642-648 (1985).

Gene Therapy

Described below are methods and compositions whereby disease symptoms can be ameliorated. The STOP-1 polypeptides (including STOP-1 polypeptide variants) described herein, antagonists and antibodies of this invnetion can be employed in accordance with the present invention by expression of each *in vivo*, which is often referred to as gene therapy. For example, STOP-1 polypeptide variants can be expressed in cells using these methods. According to one embodiment, the methods or the vectors used to express the STOP-1 polypeptides (including variants) involve the use of a stromal targeting agent to direct the vehicle containing the UNQ polypeptide or nucleic acid molecule to a desired stromal region.

There are two major approaches to getting the nucleic acid (optionally contained in a vector) into the mammal's cells: *in vivo* and *ex vivo*. For *in vivo* delivery the nucleic acid is injected directly into the mammal, usually at the sites where the STOP-1 polypeptide is required, *i.e.*, the site of synthesis of the STOP-1 polypeptide, if known, and the site (*e.g.*, wound) where biological activity of the STOP-1 polypeptide is needed. For *ex vivo* treatment, the mammal's cells are removed, the nucleic acid is introduced into these isolated cells, and the modified cells are administered to the mammal either directly or, for example, encapsulated within porous membranes that are implanted into the mammal (*see, e.g.*, U.S. Pat. Nos. 4,892,538 and 5,283,187). There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the

nucleic acid is transferred into cultured cells *in vitro*, or transferred *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, transduction, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. Transduction involves the association of a replication-defective, recombinant viral (preferably retroviral) particle with a cellular receptor, followed by introduction of the nucleic acids contained by the particle into the cell. A commonly used vector for *ex vivo* delivery of the gene is a retrovirus.

The currently preferred *in vivo* nucleic acid transfer techniques include transfection with viral or non-viral vectors (such as adenovirus, lentivirus, Herpes simplex I virus, or adeno-associated virus (AAV)) and lipid-based systems (useful lipids for lipid-mediated transfer of the gene are, for example, DOTMA, DOPE, and DC-Chol; *see, e.g.*, Tonkinson *et al.*, Cancer Investigation, 14(1): 54-65 (1996)). Such vectors are used to synthesize virus that can be used as vehicles for delivering agents, such as antagonists and nucleic acid molecules of this invention. The most preferred vectors for use in gene therapy are viruses, most preferably adenoviruses, AAV, lentiviruses, or retroviruses. A viral vector such as a retroviral vector includes at least one transcriptional promoter/enhancer or locus-defining element(s), or other elements that control gene expression by other means such as alternate splicing, nuclear RNA export, or post-translational modification of messenger. In addition, a viral vector such as a retroviral vector includes a nucleic acid molecule that, when transcribed in the presence of a gene encoding the STOP-1 polypeptide, is operably linked thereto and acts as a translation initiation sequence. Such vector constructs also include a packaging signal, long terminal repeats (LTRs) or portions thereof, and positive and negative strand primer binding sites appropriate to the virus used (if these are not already present in the viral vector). In addition, such vector typically includes a signal sequence for secretion of the STOP-1 polypeptide from a host cell in which it is placed. Preferably the signal sequence for this purpose is a mammalian signal sequence, most preferably the native signal sequence for the STOP-1 polypeptide. Optionally, the vector construct can also include a signal that directs polyadenylation, as well as one or more restriction sites and a translation termination sequence. By way of example, such vectors will typically include a 5' LTR, a tRNA binding site, a packaging signal, an origin of second-strand DNA synthesis, and a 3' LTR or a portion thereof. Other vectors can be used that are non-viral, such as cationic lipids, polylysine, and dendrimers. According to one embodiment, the vehicle has a stromal targetting agent.

In some situations, it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell-surface membrane protein or the

target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins that bind to a cell-surface membrane protein associated with endocytosis can be used for targeting and/or to facilitate uptake, *e.g.*, capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins that undergo internalization in cycling, and proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem., 262: 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA, 87: 3410-3414 (1990). For a review of the currently known gene marking and gene therapy protocols, *see*, Anderson *et al.*, Science, 256: 808-813 (1992). *See* also WO 93/25673 and the references cited therein.

Suitable gene therapy and methods for making retroviral particles and structural proteins can be found in, *e.g.*, U.S. Pat. No. 5,681,746.

Detecting STOP-1 mutations

This invention is also related to the use of the gene encoding the STOP-1 polypeptide as a diagnostic. Detection of a mutated form of the STOP-1 polypeptide can be indicative of a proclivity for developing a proliferative disorder. Detection of levels of the STOP-1 polypeptide in the tissue of a mammal over the levels of the same tissue in a normal mammal can also be indicative of proclivity of developing a proliferative disorder (below).

Individuals carrying mutations in the genes encoding a human STOP-1 polypeptide can be detected at the DNA level by a variety of techniques. Nucleic acids for diagnosis can be obtained from a mammal's cells, such as from blood, urine, saliva, tissue biopsy, and autopsy material. The genomic DNA can be used directly for detection or can be amplified enzymatically by using PCR (Saiki *et al.*, Nature, 324: 163-166 (1986)) prior to analysis. RNA or cDNA can also be used for the same purpose. As an example, PCR primers complementary to the nucleic acid encoding the STOP-1 polypeptide can be used to identify and analyze the STOP-1 polypeptide mutations. For example, deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to radiolabeled RNA encoding the STOP-1 polypeptide, or alternatively, radiolabeled antisense DNA sequences encoding the STOP-1 polypeptide. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase A digestion or by differences in melting temperatures.

Genetic testing based on DNA sequence differences can be achieved by detection of alteration in electrophoretic mobility of DNA fragments in gels with or without denaturing

agents. Small sequence deletions and insertions can be visualized by high resolution gel electrophoresis. DNA fragments of different sequences can be distinguished on denaturing formamidine gradient gels in which the mobilities of different DNA fragments are retarded in the gel at different positions according to their specific melting or partial melting temperatures. *See*, *e.g.*, Myers *et al.*, Science, 230: 1242 (1985).

Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage method, for example, Cotton *et al.*, Proc. Natl. Acad. Sci. USA, 85: 4397-4401 (1985).

Thus, the detection of a specific DNA sequence can be achieved by methods such as hybridization, RNase protection, chemical cleavage, direct DNA sequencing, or the use of restriction enzymes, *e.g.*, restriction fragment length polymorphisms (RFLP), and Southern blotting of genomic DNA.

In addition to more conventional gel-electrophoresis and DNA sequencing, mutations in the STOP-1 polypeptide can also be detected by *in situ* analysis.

Detecting STOP-1 Polypeptide or Nucleic Acid Levels

Levels of STOP-1 polypeptide or nucleic acid molecules can be detected, e.g., using the reagents disclosed herein in combination with methods known in the art, such as in situ hybridzation, RT-PCR, northern blots, western blots, or by using the Examples and reagents provided herein.

A competition assay can be employed wherein antibodies specific to the STOP-1 polypeptide are attached to a solid support and labeled STOP-1 polypeptide and a sample derived from the host are passed over the solid support and the amount of label detected attached to the solid support can be correlated to a quantity of the STOP-1 polypeptide in the sample.

In one preferred embodiment, antibodies that specifically bind STOP-1 as described herein are used to monitor STOP-1 protein levels.

Screening Assays for Drug Candidates

This invention encompasses methods of screening compounds to identify those that mimic the STOP-1 polypeptide activity (agonists) or prevent the effect of the STOP-1 polypeptide (antagonists). Generally, the STOP-1 polypeptide is exposed to the drug candidate by incubation or contact under various conditions. Screening assays for antagonist drug candidates are designed to identify compounds that specifically bind or complex with

the native STOP-1 polypeptide. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays in combination with the STOP-1 polypeptide, fragments thereof, or cells expressing the STOP-1 polypeptide or fragments thereof.

All assays for antagonists are common in that they call for contacting the drug candidate with a STOP-1 polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. For example, binding of STOP-1 polypeptide to a cancer cell or an endothelial cells in the absence or presence of the candidate antagonist can be performed in the assays described in the Examples below to evaluate whether the antagonist blocked binding of STOP-1 to the cells. In another embodiment, the STOP-1 polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, *e.g.*, on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the STOP-1 polypeptide and drying. Alternatively, an immobilized antibody, *e.g.*, a monoclonal antibody, specific for the STOP-1 polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which can be labeled by a detectable label, to the immobilized component, *e.g.*, the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, *e.g.*, by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular STOP-1 polypeptide, its interaction with that polypeptide can be assayed by methods known for detecting protein-protein interactions. Such assays include traditional approaches, such as, *e.g.*, cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song,

Nature (London), 340: 245-246 (1989); Chien *et al.*, Proc. Natl. Acad. Sci. USA, 88: 9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β-galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with binding between a STOP-1 polypeptide and another protein, including another STOP-1 polypeptide can be tested as follows: usually a reaction mixture is prepared containing the STOP-1 polypeptide and other protein under conditions and for a time allowing for the interaction and binding of the two proteins. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo can be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the other polypeptide present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the STOP-1 polypeptide and the other polypeptide.

In a proliferation assay, the STOP-1 polypeptide has the ability to stimulate the proliferation of endothelial cells in the presence of the co-mitogen ConA. Specifically, human umbilical vein endothelial cells can be obtained and cultured in 96-well flat-bottomed culture plates (Costar, Cambridge, MA) and supplemented with a reaction mixture appropriate for facilitating proliferation of the cells, the mixture containing Con-A (Calbiochem, La Jolla, CA). Con-A and the test inhibitory compound to be screened are added and after incubation at 37°C, cultures are pulsed with ^{3}H-thymidine and harvested

onto glass fiber filters (phD; Cambridge Technology, Watertown, MA). Mean $^{3-}$H-thymidine incorporation (cpm) of triplicate cultures is determined using a liquid scintillation counter (Beckman Instruments, Irvine, CA). Significant $^{3-}$(H)-thymidine incorporation indicates stimulation of endothelial cell proliferation.

According to one embodiment, the assay described above or assays as described in the Examples below are performed to test antagonists of this invention. Alternatively, antagonists can be detected by combining the STOP-1 polypeptide and a potential antagonist with cold STOP-1 polypeptide under appropriate conditions for a competitive inhibition assay. The STOP-1 polypeptide can be labeled, such as by radioactivity or a colorimetric method, such that the number of STOP-1 polypeptide molecules bound can be used to determine the effectiveness of the potential antagonist. The STOP-1 polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis

Drug candidates include anti-STOP-1 antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a drug candidate can be a closely related protein, for example, a mutated form of the STOP-1 polypeptide that competitively inhibits the action of the STOP-1 polypeptide.

Administration Protocols, Schedules, Doses, and Formulations

The molecules herein and antagonists thereto are pharmaceutically useful as a prophylactic and therapeutic agent for various disorders and diseases as set forth above.

Therapeutic compositions of the polypeptides, antibodies or antagonists of this invention are prepared for storage by mixing the desired molecule having the appropriate degree of purity with optional pharmaceutically acceptable carriers, excipients, or stabilizers (Remington's Pharmaceutical Sciences, 16th edition, Osol, A. ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol;

cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

Additional examples of such carriers include ion exchangers, alumina, aluminum stearate, lecithin, serum proteins, such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, water, salts, or electrolytes such as protamine sulfate, disodium hydrogen phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, cellulose-based substances, and polyethylene glycol. Carriers for topical or gel-based forms of agonist or antagonist include polysaccharides such as sodium carboxymethylcellulose or methylcellulose, polyvinylpyrrolidone, polyacrylates, polyoxyethylene-polyoxypropylene-block polymers, polyethylene glycol, and wood wax alcohols. For all administrations, conventional depot forms are suitably used. Such forms include, for example, microcapsules, nano-capsules, liposomes, plasters, inhalation forms, nose sprays, sublingual tablets, and sustained-release preparations. The STOP-1 polypeptides or agonists or antagonists will typically be formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml.

Another formulation comprises incorporating a STOP-1 polypeptide or agonist or antagonist thereof into formed articles. Such articles can be used in modulating endothelial cell growth and angiogenesis. In addition, tumor invasion and metastasis can be modulated with these articles.

STOP-1 polypeptides or agonists or antagonists to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution. STOP-1 polypeptides ordinarily will be stored in lyophilized form or in solution if administered systemically. If in lyophilized form, the STOP-1 polypeptide or agonist or antagonist thereto is typically formulated in combination with other ingredients for reconstitution with an appropriate diluent at the time for use. An example of a liquid formulation of a STOP-1 polypeptide or agonist or antagonist is a sterile, clear, colorless unpreserved solution filled in a single-dose

vial for subcutaneous injection. Preserved pharmaceutical compositions suitable for repeated use can contain, for example, depending mainly on the indication and type of polypeptide:

a. STOP-1 polypeptide or agonist or antagonist thereto;
b. a buffer capable of maintaining the pH in a range of maximum stability of the polypeptide or other molecule in solution, preferably about 4-8;
c. a detergent/surfactant primarily to stabilize the polypeptide or molecule against agitation-induced aggregation;
d. an isotonifier;
e. a preservative selected from the group of phenol, benzyl alcohol and a benzethonium halide, *e.g.*, chloride; and
f. water.

If the detergent employed is non-ionic, it can, for example, be polysorbates (*e.g.*, POLYSORBATE™ (TWEEN™) 20, 80, etc.) or poloxamers (*e.g.*, POLOXAMER™ 188). The use of non-ionic surfactants permits the formulation to be exposed to shear surface stresses without causing denaturation of the polypeptide. Further, such surfactant-containing formulations can be employed in aerosol devices such as those used in a pulmonary dosing, and needleless jet injector guns (*see*, *e.g.*, EP 257,956).

An isotonifier can be present to ensure isotonicity of a liquid composition of the STOP-1 polypeptide or agonist or antagonist thereto, and includes polyhydric sugar alcohols, preferably trihydric or higher sugar alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol, and mannitol. These sugar alcohols can be used alone or in combination. Alternatively, sodium chloride or other appropriate inorganic salts can be used to render the solutions isotonic.

The buffer can, for example, be an acetate, citrate, succinate, or phosphate buffer depending on the pH desired. The pH of one type of liquid formulation of this invention is buffered in the range of about 4 to 8, preferably about physiological pH.

The preservatives phenol, benzyl alcohol and benzethonium halides, *e.g.*, chloride, are known antimicrobial agents that can be employed.

Therapeutic STOP-1 polypeptide or antibody compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle. The formulations are preferably administered as repeated intravenous (i.v.), subcutaneous (s.c.), or intramuscular (i.m.) injections, or as aerosol formulations suitable for intranasal or intrapulmonary delivery (for intrapulmonary delivery *see*, *e.g.*, EP 257,956).

STOP-1 polypeptides or antibodies can also be administered in the form of sustained-released preparations. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the protein, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (*e.g.*, poly(2-hydroxyethyl-methacrylate) as described by Langer *et al.*, J. Biomed. Mater. Res., 15: 167-277 (1981) and Langer, Chem. Tech., 12: 98-105 (1982) or poly(vinylalcohol)), polylactides (U.S. Patent No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, Biopolymers, 22: 547-556 (1983)), non-degradable ethylene-vinyl acetate (Langer *et al.*, *supra*), degradable lactic acid-glycolic acid copolymers such as the Lupron Depot™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid (EP 133,988).

While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated proteins remain in the body for a long time, they can denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for protein stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization can be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

Sustained-release STOP-1 polypeptide and antibody compositions also include liposomally entrapped STOP-1 polypeptides. Liposomes containing the STOP-1 polypeptide are prepared by methods known *per se*: DE 3,218,121; Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688-3692 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese patent application 83-118008; U.S. Patent Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. % cholesterol, the selected proportion being adjusted for the optimal therapy.

The therapeutically effective dose of a STOP-1 polypeptide or antagonist thereto will, of course, vary depending on such factors as the proliferative disorder to be treated (including prevention), the method of administration, the type of compound being used for treatment,

any co-therapy involved, the patient's age, weight, general medical condition, medical history, etc., and its determination is well within the skill of a practicing physician. Accordingly, it will be necessary for the therapist to titer the dosage and modify the route of administration as required to obtain the maximal therapeutic effect. The clinician will administer the STOP-1 polypeptide or antagonist until a dosage is reached that achieves the desired effect for treatment of the condition in question. For example, if the objective is the treatment of cancer, the amount would be one that inhibits the growth of the cancer.

With the above guidelines, the effective dose generally is within the range of from about 0.001 to about 1.0 mg/kg, more preferably about 0.01-1.0 mg/kg, most preferably about 0.01-0.1 mg/kg.

For non-oral use in treating proliferative disorders, it is advantageous to administer the STOP-1 polypeptide or antagonist thereto in the form of an injection at about 0.01 to 50 mg, preferably about 0.05 to 20 mg, most preferably 1 to 20 mg, per kg body weight, 1 to 3 times daily by intravenous injection. For oral administration, a molecule based on the STOP-1 polypeptide is preferably administered at about 5 mg to 1 g, preferably about 10 to 100 mg, per kg body weight, 1 to 3 times daily. It should be appreciated that endotoxin contamination should be kept minimally at a safe level, for example, less than 0.5 ng/mg protein. Moreover, for human administration, the formulations preferably meet sterility, pyrogenicity, general safety, and purity as required by FDA Office and Biologics standards.

The dosage regimen of a pharmaceutical composition containing the STOP-1 polypeptide to be used in tissue regeneration will be determined by the attending physician considering various factors that modify the action of the polypeptides, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration, and other clinical factors. The dosage can vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF-I, to the final composition can also affect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations, and tetracycline labeling.

The route of STOP-1 polypeptide or antagonist or agonist administration is in accord with known methods, *e.g.*, by injection or infusion by intravenous, intramuscular, intracerebral, intraperitoneal, intracerobrospinal, subcutaneous, intraocular, intraarticular, intrasynovial, intrathecal, oral, topical, or inhalation routes, or by sustained-release systems

as noted below. The STOP-1 polypeptide or agonist or antagonists thereof also are suitably administered by intratumoral, peritumoral, intralesional, or perilesional routes, to exert local as well as systemic therapeutic effects. The intraperitoneal route is expected to be particularly useful, for example, in the treatment of ovarian tumors.

If a peptide or small molecule is employed as an antagonist or agonist, it is preferably administered orally or non-orally in the form of a liquid or solid to mammals.

Examples of pharmacologically acceptable salts of molecules that form salts and are useful hereunder include alkali metal salts (*e.g.*, sodium salt, potassium salt), alkaline earth metal salts (*e.g.*, calcium salt, magnesium salt), ammonium salts, organic base salts (*e.g.*, pyridine salt, triethylamine salt), inorganic acid salts (*e.g.*, hydrochloride, sulfate, nitrate), and salts of organic acid (*e.g.*, acetate, oxalate, p-toluenesulfonate).

For compositions herein that are useful for bone, cartilage, tendon, or ligament regeneration, the therapeutic method includes administering the composition topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use is in a pyrogen-free, physiologically acceptable form. Further, the composition can desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage, or tissue damage. Topical administration can be suitable for wound healing and tissue repair. Preferably, for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and preferably capable of being resorbed into the body. Such matrices can be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance, and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions can be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid, and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices can be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics can be altered in

composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

One specific embodiment is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the polypeptide compositions from disassociating from the matrix.

One suitable family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydoxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, one preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer, and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt%, based on total formulation weight, which represents the amount necessary to prevent desorption of the polypeptide (or its antagonist) from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the polypeptide (or its antagonist) the opportunity to assist the osteogenic activity of the progenitor cells.

Combination Therapies

The effectiveness of the STOP-1 polypeptide or an agonist or antagonist thereof in preventing or treating the disorder in question can be improved by administering the active agent serially or in combination with another agent that is effective for those purposes, either in the same composition or as separate compositions.

For example, for treatment of cell proliferative disorders, STOP-1 polypeptide antagonist therapy can be combined with the administration of other inhibitors of cell proliferation, such as cytotoxic agents.

In addition, STOP-1 polypeptide antagonists used to treat cancer can be combined with cytotoxic, chemotherapeutic, or growth-inhibitory agents as identified above. Also, for cancer treatment, the STOP-1 polypeptide antagonist thereof is suitably administered serially or in combination with radiological treatments, whether involving irradiation or administration of radioactive substances.

If the treating is for cancer, it may be desirable also to administer antibodies against other tumor-associated antigens, such as antibodies that bind to one or more of the ErbB2, EGFR, ErbB3, ErbB4, or VEGF receptor(s). Alternatively, or in addition, two or more antibodies binding the same or two or more different antigens disclosed herein may be co-administered to the patient. Sometimes, it may be beneficial also to administer one or more cytokines to the patient. In one preferred embodiment, the antagonist antibodies herein are co-administered with a growth-inhibitory agent. For example, the growth-inhibitory agent may be administered first, followed by an antagonist antibody of the present invention. However, simultaneous administration or administration of the antagonist antibody of the present invention first is also contemplated. Suitable dosages for the growth-inhibitory agent are those presently used and may be lowered due to the combined action (synergy) of the growth-inhibitory agent and the antibody herein.

In one embodiment, vascularization of tumors is attacked in combination therapy. The antagonist antibodies of this invention and another antibody (e.g., anti-VEGF) are administered to tumor-bearing patients at therapeutically effective doses as determined, for example, by observing necrosis of the tumor or its metastatic foci, if any. This therapy is continued until such time as no further beneficial effect is observed or clinical examination shows no trace of the tumor or any metastatic foci. Then TNF is administered, alone or in combination with an auxiliary agent such as alpha-, beta-, or gamma-interferon, anti-HER2 antibody, heregulin, anti-heregulin antibody, D-factor, interleukin-1 (IL-1), interleukin-2 (IL-2), granulocyte-macrophage colony stimulating factor (GM-CSF), or agents that promote microvascular coagulation in tumors, such as anti-protein C antibody, anti-protein S antibody, or C4b binding protein (see, WO 91/01753, published 21 February 1991), or heat or radiation.

The effective amounts of the therapeutic agents administered in combination with the STOP-1 polypeptide or antagonist thereof will be at the physician's or veterinarian's discretion. Dosage administration and adjustment is done to achieve maximal management of the conditions to be treated. The dose will additionally depend on such factors as the type of the therapeutic agent to be used and the specific patient being treated. Typically, the amount employed will be the same dose as that used, if the given therapeutic agent is administered without the STOP-1 polypeptide.

Articles of Manufacture

An article of manufacture such as a kit containing the STOP-1 polypeptide or agonists or antagonists thereof useful for the diagnosis or treatment of the disorders described above comprises at least a container and a label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers can be formed from a variety of materials such as glass or plastic. The container holds a composition that is effective for diagnosing or treating the condition and can have a sterile access port (for example, the container can be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is the STOP-1 polypeptide or an agonist or antagonist thereto. The label on, or associated with, the container indicates that the composition is used for diagnosing or treating the condition of choice. The article of manufacture can further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution, and dextrose solution. It can further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use. The article of manufacture can also comprise a second or third container with another active agent as described above.

Polyclonal Antibodies

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent can include the STOP-1 polypeptide or a fusion protein thereof. It can be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include, but are not limited to, keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants that can be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A or synthetic trehalose dicorynomycolate). The immunization protocol can be selected by one skilled in the art without undue experimentation.

Monoclonal Antibodies

Anti-STOP-1 antibodies can be monoclonal antibodies. Monoclonal antibodies can be prepared, e.g., using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975) or can be made by recombinant DNA methods (US Patent No. 4,816,567) or can be produced by the methods described herein in the Example section. In a hybridoma method, a mouse, hamster, or other appropriate host animal is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized *in vitro*.

The immunizing agent will typically include the STOP-1 polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell. Goding, Monoclonal Antibodies: Principles and Practice (New York: Academic Press, 1986), pp. 59-103. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high-level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies. Kozbor, J. Immunol., 133:3001 (1984); Brodeur *et al.*, Monoclonal Antibody Production Techniques and Applications (Marcel Dekker, Inc.: New York, 1987) pp. 51-63.

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the STOP-1 polypeptide. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is

determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Goding, *supra*. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy- and light-chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison *et al.*, *supra*) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies can be monovalent antibodies. Methods for preparing monovalent antibodies are known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy-chain crosslinking.

Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly Fab fragments, can be accomplished using techniques known in the art.

Human and Humanized Antibodies

The anti-STOP-1 antibodies can further comprise humanized antibodies or human antibodies. Humanized forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$, or other antigen-binding subsequences of antibodies) that contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a CDR of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin, and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody preferably also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Jones *et al.*, Nature, 321: 522-525 (1986); Riechmann *et al.*, Nature, 332: 323-329 (1988); Presta, Curr. Op. Struct. Biol., 2:593-596 (1992).

Methods for humanizing non-human antibodies are known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*, Nature, 321: 522-525 (1986); Riechmann *et al.*, Nature, 332: 323-327 (1988); Verhoeyen *et al.*, Science, 239: 1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact

human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

As an alternative to humanization, human antibodies can be generated. For example, it is now possible to produce transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (JH) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array into such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g., Jakobovits et al., Proc. Natl. Acad. Sci. USA, 90:2551 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggemann et al., Year in Immuno., 7:33 (1993); U.S. Patent Nos. 5,545,806, 5,569,825, 5,591,669 (all of GenPharm); 5,545,807; and WO 97/17852. Alternatively, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed that closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; and 5,661,016, and in the following scientific publications: Marks *et al.*, Bio/Technology, 10: 779-783 (1992); Lonberg *et al.*, Nature, 368: 856-859 (1994); Morrison, Nature, 368: 812-813 (1994); Fishwild *et al.*, Nature Biotechnology, 14: 845-851 (1996); Neuberger, Nature Biotechnology, 14: 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol., 13: 65-93 (1995).

Alternatively, phage display technology (McCafferty et al., Nature 348:552-553 [1990]) can be used to produce human antibodies and antibody fragments in vitro, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. According to this technique, antibody V domain genes are cloned in-frame into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody

exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats, reviewed in, e.g., Johnson, Kevin S. and Chiswell, David J., Current Opinion in Structural Biology 3:564-571 (1993). Several sources of V-gene segments can be used for phage display. Clackson et al., Nature, 352:624-628 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens (including self-antigens) can be isolated essentially following the techniques described by Marks et al., J. Mol. Biol. 222:581-597 (1991), or Griffith et al., EMBO J. 12:725-734 (1993). See, also, U.S. Patent Nos. 5,565,332 and 5,573,905.

As discussed above, human antibodies may also be generated by in vitro activated B cells (see U.S. Patents 5,567,610 and 5,229,275).

Human antibodies can also be produced using various techniques known in the art, including phage display libraries. Hoogenboom and Winter, J. Mol. Biol., 227: 381 (1991); Marks *et al.*, J. Mol. Biol., 222: 581 (1991). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies. Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner *et al.*, J. Immunol., 147(1): 86-95 (1991).

Bispecific anti-STOP-1 Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the STOP-1 polypeptide, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit. For example, the cell-surface protein can be a natural killer (NK) cell receptor. Thus, according to one embodiment, a bispecific antibody of this invention can bind STOP-1 and bind a NK cell and, optionally, activate the NK cell. According to another embodiment, a bispecific antibody of this invention can bind STOP-1 and binds to a stromal tissue compared to other tissue (e.g., stromal targeting agent).

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities. Milstein and Cuello, Nature, 305: 537-539 (1983). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas)

produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, EMBO J., 10: 3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant-domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies, *see*, for example, Suresh *et al.*, Methods in Enzymology, 121: 210 (1986).

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol., 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a VH connected to a VL by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber et al., J. Immunol., 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al. J. Immunol. 147: 60 (1991)

Heteroconjugate Antibodies

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune-system cells to unwanted cells

(U.S. Patent No. 4,676,980), and for treatment of HIV infection. WO 91/00360; WO 92/200373; EP 03089. It is contemplated that the antibodies can be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide-exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). *See*, Caron *et al.*, J. Exp. Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.*, Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. *See*, Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).

Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the

tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. *See*, WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

Immunoliposomes

The antibodies disclosed herein can also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. *See*, Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a STOP-1 polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders as noted above and below in the form of pharmaceutical compositions.

Lipofectins or liposomes can be used to deliver the polypeptides, nucleic acid molecules, antibodies, antagonists or composition of this invention into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. *See, e.g.,* Marasco *et al.,* Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993).

The formulation herein can also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition can comprise an agent that enhances its function, such as, for example, a cytotoxic agent, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients can also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra.*

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations can be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.,* films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable

ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT ™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they can denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization can be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

Methods of Treatment using the anti-STOP-1 Antibody

It is contemplated that the antibodies to a STOP-1 polypeptide can be used to treat various proliferative disorders and diseases complicated or related to angiogenesis as noted above.

The antibodies are administered to a mammal, preferably a human, in accord with known methods, such as intravenous administration as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. Intravenous administration of the antibody is preferred.

Other therapeutic regimens can be combined with the administration of the antibodies of the instant invention as noted above. For example, if the antibodies are to treat cancer, the patient to be treated with such antibodies can also receive radiation therapy. Alternatively, or in addition, a chemotherapeutic agent can be administered to the patient. Preparation and dosing schedules for such chemotherapeutic agents can be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in Chemotherapy Service, Ed., M.C. Perry (Williams & Wilkins: Baltimore, MD, 1992). The chemotherapeutic agent can precede, or follow administration of the antibody, or can be given simultaneously therewith. The antibody can be combined with an anti-estrogen compound such as tamoxifen or

EVISTA™ or an anti-progesterone such as onapristone (*see*, EP 616812) in dosages known for such molecules.

If the antibodies are used for treating cancer, they can be, optionally, administer with antibodies against other tumor-associated antigens, such as antibodies that bind to one or more of the ErbB2, EGFR, ErbB3, ErbB4, or VEGF receptor(s). These also include the agents set forth above. Also, the antibody is suitably administered serially or in combination with radiological treatments, whether involving irradiation or administration of radioactive substances. Alternatively, or in addition, two or more antibodies binding the same or two or more different antigens disclosed herein can be co-administered to the patient. In a preferred embodiment, the antibodies herein are co-administered with a growth-inhibitory agent. For example, the growth-inhibitory agent can be administered first, followed by an antibody of the present invention. However, simultaneous administration or administration of the antibody of the present invention first is also contemplated. Suitable dosages for the growth-inhibitory agent are those presently used and can be lowered due to the combined action (synergy) of the growth-inhibitory agent and the antibody herein.

In one embodiment, vascularization of tumors is attacked in combination therapy. The anti-STOP-1 polypeptide antibody and another antibody (*e.g.*, anti-VEGF) are administered to tumor-bearing patients at therapeutically effective doses as determined, for example, by observing necrosis of the tumor or its metastatic foci, if any. This therapy is continued until such time as no further beneficial effect is observed or clinical examination shows no trace of the tumor or any metastatic foci. Then TNF is administered, alone or in combination with an auxiliary agent such as alpha-, beta-, or gamma-interferon, anti-HER2 antibody, heregulin, anti-heregulin antibody, D-factor, interleukin-1 (IL-1), interleukin-2 (IL-2), granulocyte-macrophage colony stimulating factor (GM-CSF), or agents that promote microvascular coagulation in tumors, (such as anti-protein C antibody, anti-protein S antibody, or C4b binding protein, *see*, WO 91/01753, published 21 February 1991), or heat or radiation.

Since the auxiliary agents will vary in their effectiveness, it can be desirable to compare their impact on the tumor by matrix screening in conventional fashion. The administration of anti-STOP-1 polypeptide antibody and TNF is repeated until the desired clinical effect is achieved. Alternatively, the anti-STOP-1 polypeptide antibody is administered together with TNF and, optionally, auxiliary agent(s). In instances where solid tumors are found in the limbs or in other locations susceptible to isolation from the general circulation, the therapeutic agents described herein are administered to the isolated tumor or

organ. In other embodiments, a FGF or PDGF antagonist, such as an anti-FGF or an anti-PDGF neutralizing antibody, is administered to the patient in conjunction with the anti-STOP-1 polypeptide antibody. Treatment with anti-STOP-1 polypeptide antibodies preferably can be suspended during periods of wound healing or desirable neovascularization.

For the prevention or treatment of a proliferative disorder, the appropriate dosage of an antibody herein will depend on the type of disorder to be treated, as defined above, the severity and course of the disease, whether the antibody is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, and the discretion of the attending physician. The antibody is suitably administered to the patient at one time or over a series of treatments.

For example, depending on the type and severity of the disorder, about 1 ug/kg to 50 mg/kg (*e.g.*, 0.1-20 mg/kg) of antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A typical daily or weekly dosage might range from about 1 ug/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is repeated or sustained until a desired suppression of disorder symptoms occurs. However, other dosage regimens can be useful. The progress of this therapy is easily monitored by conventional techniques and assays, including, for example, radiographic tumor imaging.

Articles of Manufacture with Antibodies

An article of manufacture containing a container with the antibody and a label is also provided. Such articles are described above, wherein the active agent is an anti-STOP-1 antibody.

Diagnosis and Prognosis of Tumors using Antibodies

If the indication for which the antibodies are used is cancer, while cell-surface proteins, such as growth receptors over expressed in certain tumors, are excellent targets for drug candidates or tumor (*e.g.*, cancer) treatment, the same proteins along with STOP-1 polypeptides find additional use in the diagnosis and prognosis of tumors. For example, antibodies directed against the STOP-1 polypeptides can be used as tumor diagnostics or prognostics.

For example, antibodies, including antibody fragments, can be used qualitatively or quantitatively to detect the expression of genes including the gene encoding the STOP-1

polypeptide. The antibody preferably is equipped with a detectable, *e.g.*, fluorescent label, and binding can be monitored by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. Such binding assays are performed essentially as described above.

In situ detection of antibody binding to the marker gene products can be performed, for example, by immunofluorescence or immunoelectron microscopy. For this purpose, a histological specimen is removed from the patient, and a labeled antibody is applied to it, preferably by overlaying the antibody on a biological sample. This procedure also allows for determining the distribution of the marker gene product in the tissue examined. It will be apparent to those skilled in the art that a wide variety of histological methods are readily available for *in situ* detection.

All publications (including patents and patent applications) cited herein are hereby incorporated in their entirety by reference.

The deposits herein were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposits for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposits to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 U.S.C. 122 and the Commissioner's rules pursuant to thereto (including 37 C.F.R. 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposits should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

Commercially available reagents referred to in the Examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following Examples, and throughout the specification, by ATCC accession numbers is the

American Type Culture Collection, Manassas, VA. Unless otherwise noted, the present invention uses standard procedures of recombinant DNA technology, such as those described hereinabove and in the following textbooks: Sambrook *et al., supra*; Ausubel *et al.,* Current Protocols in Molecular Biology (Green Publishing Associates and Wiley Interscience, N.Y., 1989); Innis *et al.,* PCR Protocols: A Guide to Methods and Applications (Academic Press, Inc.: N.Y., 1990); Harlow *et al.,* Antibodies: A Laboratory Manual (Cold Spring Harbor Press: Cold Spring Harbor, 1988); Gait, Oligonucleotide Synthesis (IRL Press: Oxford, 1984); Freshney, Animal Cell Culture, 1987; Coligan *et al.,* Current Protocols in Immunology, 1991.

Throughout this specification and claims, the word "comprise," or variations such as "comprises" or "comprising," will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

The foregoing written description is considered to be sufficient to enable one skilled in the art to practice the invention. The following Examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

EXPERIMENTAL SECTION

Example 1 - - STOP-1 is conserved in evolution

Nucleic acid molecules containing human, mouse and zebra fish STOP-1 were obtained by using PCR. Sequences with homology to human, mouse and zebra fish STOP-1 can be found in the Genebank database mouse EST: AK003674; chicken ESTs: A1585129, AL585130; rice fish ESTs: BJ490431, BJ498080, BJ510203, BJ504730; and zebra fish ESTs: AL727874, AW595388; and HGT AL844521. Nucleic acid sequences of human, mouse, rice fish, zebra fish and chicken STOP-1 nucleic acid molecules are described in SEQ ID NOS: 1,3, 5, 7 and 9, respectively. Their amino acid sequences are recited as SEQ ID NOS: 2, 4, 6, 8 and 10, respectively, and FIG.1. The cDNAs of human STOP-1 were deposited under the terms of the Budapest Treaty with the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209, USA as described below:

Species	Material	Deposit No.	Deposit Date

Human	76393-1664	203323	October 6, 1998
Human	h762HIP	PTA-5019	February 21, 2003

Amino acid alignment of STOP-1 among several higher vertebrate species (human, mouse, chicken, zebra and rice fishes) shows a high degree of conservation, in particular, parts of the C-terminal domain including the triple helix domain (FIG.1). In the consensus sequence, an asterick indicates residues conserved in all species. A blackened circle indicates residues that are conserved in most species.

FIG. 2 shows a human STOP-1 protein. The boxed sequence indicates the signal cleavage site. The Triple Helix Domain is underlined.

Example 2 - - STOP-1 is overexpressed in tumors

A proprietary database containing gene expression information from microarrays (GeneExpress®, GeneLogic Inc., Gaithersburg, MD) was analyzed for the expression of *STOP-1* mRNA in various tumors (BLIST analysis, proprietary software written an developed at Genentech, Inc. for use with the GeneExpress® database). Some of the types of tissues analyzed included: adipose, adrenal, blood vessel, bone breast, cervix, CNS, colorectal endometrium, esophagus, gall bladder, head and neck, heart, hematopoetic, kidney, liver, lung, lymphoid, muscle, myometrium, euroendocrine, ovary, pancreas, prostate, skin, small intestine, soft tissue, stomach, testis, thymus, thyroid and urinary and normal tissues (breast, colon, lung, ovarian and kidney). STOP-1 mRNA levels were observed to be especially elevated in bone, breast, cervix, colorectal, endometrium, esophagus, glioma, head & neck, kidney, lung, euroendocrine, ovary, pancreas, skin, soft tissue, stomach, thyroid and urinary tumors.

RNA expression levels were also determined by reverse transcription (RT) and polymerase chain reaction (PCR) amplification of the specific target, STOP-1 (SEQ ID NO:1), in total RNA from a variety of tumors and normal tissues (breast, colon, lung, ovarian and kidney). Tissues were obtained by the Genentech pathology Department and RNA prepared by cesium chloride centrifugation.

One step RT-PCR amplification reactions consisted of 10x Buffer A (Applied Biosystems), 10 Units RNase inhibitor, 200uM dATP, dCTP, dGTP, dTTP, 5mM MgC_{12}, 1.25 Units Taq Gold Polymerase, 25 Units MULV reverse transcriptase (PE Biosystems), 50ng total RNA, 200 nM gene-specific hybridization probe (FAM-

CATCCAGTAGAAGCATCTCCTTTTGGGTAA-TAMRA) (SEQ ID NO:23), 300 nM gene-specific forward primer (GGGTTGGCACTTGTTCAGA) (SEQ ID NO:24) and 300 nM gene-specific reverse primer (CAATAATGATGCGAGAAACTGAAT) (SEQ ID NO:25) in water to a final volume of 50uL. Thermal cycling conditions were as follows: 1) 48°C, 30minutes; 2) 95°C, 10 minutes; and 3) 40 cycles of 95°C, 15 seconds and 60°C, 1minute using an ABI 7700 Sequence Detection System. Transcript levels were normalized to the housekeeping genes GAPDH or RPL19.

Taqman analysis confirmed the overexpression of STOP-1 mRNA in these tumors, especially pancreas, kidney, breast, lung, ovarian, colorectal tumors, soft tissue, stomach thyroid and urinary tumors. Fourteen out of eighteen breast and colon tumor samples showed five to twenty-seven fold overexpression as compared with normal samples. Other tumor types also showed an increase although to a lesser degree. Those tumor types included adrenal, bone, cervical, endometrium, esophagus, head & neck, kidney, liver and euroendocrine.

Example 3 - - In Situ Hybridization Studies

(a) Probe synthesis

12.0μl (125mCi) of [alpha-^{33}P]UTP (NEN/Perkin-Elmer NEG307H) was speed vac dried in a siliconized 1.5 μl microfuge (Eppendorf) tube. To each tube having dried ^{33}P-UTP, the following reagents were added and incubated for 1 hour in a 37 °C water bath:

2.0 μl Transcription Optimized 5X Buffer (Promega, P1181)

2.0 μl SQ H2O

1.0 μl DTT, 100mM (Promega, P1171)

2.0 μl rNTP mix, 2.5mM [10μl each of 10mM rATP (Promega, P113B), rCTP (Promega, P114B) & GTP (Promega, P115B)+ 10μl Nuclease-Free H_2O (Promega, P1193)]

1.0 μl RNasin Ribonuclease Inhibitor (Promega, N2511)

1.0 μl DNA Template (1ug of linear PCR-amplified DNA template encoding a portion of the human STOP-1 coding sequence flanked by the RNA polymerase promoter sequences of bacteriophage T7 on the upper strand for sense control probe transcription and of bacteriophageT3 on the bottom strand for antisense probe transcription)

The sequence in the transcription reaction with the sense and anti-sense probes was: 5'-GGGAGCCATG CGACCCCAGG GCCCCGCCGC CTCCCCGCAG CGGCTCCGCG GCCTCCTGCT GCTCCTGCTG CTGCAGCTGC CCGCGCCGTC GAGCGCCTCT GAGATCCCCA AGGGGAAGCA AAAGGCGCAG CTCCGGCAGA GGGAGGTGGT GGACCTGTAT AATGGAATGT GCTTACAAGG GCCAGCAGGA GTGCCTGGTC GAGACGGGAG CCCTGGGGCC AATGTTATTC CGGGTACACC TGGGATCCCA GGTCGGGATG GATTCA - 3' (SEQ ID NO:26)

1.0 µl RNA Polymerase T3 (Promega, P2083) for antisense probes or
1.0 µl RNA Polymerase T7 (Promega, P2075) for sense probes.

Next, 1µl of RQ1 RNase-Free DNase (Promega, M6101) was added to the Eppendorf tube containing the radioactively-labeled RNA probe and the reaction was further incubated for 15 minutes at 37°C. This step degraded the DNA template in the reaction. To stop the degradation reaction, 90 µl TE (10mM Tris pH 7.6 / 1mM EDTA pH 8.0) was added to the Eppendorf tube. Unincorporated nucleotides are removed using an RNeasy Mini Kit (Qiagen 74104, Germantown, MD).

The probe yield was determined by pipetting onto separate rounds of DE81 ion exchange paper (Whatman, 3658 325) 1 µl prefiltered probe and1 µl of probe following filtration. The samples are immersed in 6 ml of Biofluor (Packard, 6NEF-961) in scintillation vials (Wheaton Scientific, 986701) and counted on Beckman LS 6500.

Next, the probe was analyzed on a 6% Polyacrylamide TBE/Urea gel (Novex EC6865, Invitrogen, Carlsbad, CA) to confirm that the transcript was of the proper length. $1x10^6$ cpm of probe or 2 µl of Novagen Perfect RNA marker 0.1-1kb (Novagen 69924-1) was added to 3 µl TBE/Urea Sample Buffer (Novex, LC6876). The RNAs were denatured on 95°C heat blocks for 3 minutes and then immediately chilled on ice. The samples were run at 180-250 volts for 45 minutes. The gel was exposed for 1 hour to Biomax MS film (Kodax, 829 4985) with an intensifying screen in -70°C freezer.

(b) In situ hybridization

In situ hybridization analysis was performed initially on sections of normal and tumor tissues. The slides were hybridized to human STOP-1 sense and anti-sense RNA probes using the techniques described below. Further analysis was conducted on sections of tissue microarrays (TMAs) containing numerous normal and tumor tissue specimens. The TMA sections were hybridized exclusively with antisense RNA probes.

The slides were baked in an oven to adhere tissue to glass at 37°C overnight followed by 65°C for 30 minutes. The sections were deparaffinized in a Leica Autostainer XL (Leica, Deerfield, IL) by incubating 3 times for 5 minutes each in Xylenes (Richard Allen, Kalamazoo, MI) then rehydrating through a graded ethanol series to distilled water. Slides were then washed twice in 2X SSC (0.3 M NaCl, 0.030 M NaCitrate, pH 7.0) for 5 minutes each time. The slides were treated for 15 minutes in a 20 µg/ml Proteinase K (Roche Diagnostics, Indianapolis, IN) in 10 mM Tris pH 8.0/ 0.5 M NaCl solution at 37°C and washed for 10 minutes in 0.5X SSC (0.075 M NaCl, 0.007 M NaCitrate, pH 7.0). The slides were dehydrated with an ethanol gradient (70%- 95%- 100%) and air-dried. The slides were covered with 100 µl hybridization buffer (50% formamide, 10% dextran sulfate, and 2X SSC) and prehybridized for 1-4 hours at 42°C. The [^{33}P]-labeled single-stranded STOP-1 probe (anti-sense orientation) referenced above at a concentration of 2 x 10^6 cpm was dissolved in 100 µl of hybridization buffer containing 1 mg/ml tRNA and added to the prehybridization buffer on one of the slides, mixed well, covered with coverslip, and allowed to hybridize overnight at 55°C in a sealed humidified container.

The foregoing hybridization procedure was performed on another slide from the same tissue block using the same [^{33}P]-labeled single-stranded STOP-1 probe in the sense orientation.

After hybridization, the slides were washed twice for 10 minutes in 2X SSC containing 1 mM EDTA at room temperature, and then incubated for 30 minutes at 37°C in 20 µg/mL RNase A in 10 mM Tris pH 8, 0.5 M NaCl. The slides were washed for 10 minutes in 2X SSC containing 1 mM EDTA at room temperature, then washed 4 times for 30 minutes each in 0.1X SSC containing 1 mM EDTA at 55°C, and then washed in 0.5X SSC for 10 minutes at room temperature. The slides were dehydrated for 2 minutes each in 50%, 70%, and 90% ethanol containing 0.3M ammonium acetate, and allowed to dry in the air.

Slides were apposed to X-ray film (Biomax MR Film, Kodax, 870 1302) for 16 hours to obtain a preliminary assessment of the success of the experiment. Slides were then dipped in NTB2 Emulsion (Kodax, 165 4433) [1:1 dilution with H_20], allowed to dry overnight in

complete darkness, transferred into light tight boxes with desiccant and allowed to expose for 4 weeks. After 4 weeks, slides were developed using D-19 developer [1:1 dilution with H_20] for 3 minutes at 15°C, rinsed and fixed in GBX fixer for 6 minutes at 15°C. Slides were counterstained with hematoxylin and eosin prior to examination by a pathologist.

Table 7 shows the results of the in situ hybridization experiments:

TABLE 7

TISSUE TYPE	NORMAL TISSUE (# of positive/total)	TUMOR TISSUE (# of positive/total)
Lung	2/16 adult	41/49 adenocarcinoma 27/30 squamous cell carcinoma 1/1 large cell carcinoma 2/5 lung neuroendocrine tumor Cell Lines - all tested negative Calu-6 (lung carcinoma anaplastic) SK-MES cell (squamous cell lung) H322 A549 (lung carcinoma) H522
Breast	0/6 adult	2/14 adult
Colon	0/5 adult	4/8 adult
Small Intestine	1/5 adult	-
Pancreas	0/2 adult	3/5 adult
Heart	0/2 fetal 0/4 adult	- -
Placenta	0/5 adult	-
Aorta	0/1 adult	-
Blood Vessel	0/1 adult	-
Thymus	0/1 adult	-
Trachea	0/1 adult	-

Liver	0/3 adult	2/4 adult hepatocellular carcinoma
Thyroid	1/3 adult	-
Skin	1/1 adult in follicle and dermis	4/4 adult melanoma
Stomach	0/3 adult	-
Brain	0/4 adult	-
Spleen	0/4 adult	-
Lymph Node	0/3 adult	0/4 lymphomas adult
Prostate	0/3 adult	0/1 lymphomas adult
Ovary	1/1 adult	2/2 adult
Urinary Bladder	0/1 adult	3/3 transitional cell carcinomas
Gall Bladder	0/1 adult	-
Kidney	0/2 adult	0/4 adult
Adrenal	0/1 adult	-
Endometrium	-	2/3 adult
Cartilage	-	0/1 chondrosarcoma
Adipose	-	0/1 liposarcoma
Fetal Tissues	0/1 aorta, blood vessel, thymus, trachea, liver, lung	-

The in situ hybridization experiments showed that most normal samples tested negative for STOP-1 mRNA. On the other hand, an astonishingly high number of lung tumors, colon tumors, pancreatic tumors, hepatocellular carcinomas, melanomas, ovarian cancers, endometrial cancers and urinary bladder transitional cell carcinomas showed significant STOP-1 mRNA expression. Furthermore, STOP-1 mRNA was mainly expressed in the stroma (e.g., lung squamous cell carcinomas, adenocarcinomas, breast carcinoma) and not the epithelial compartments of most tumors with the exception of the melanomas which expressed STOP-1 mRNA in the neoplastic cells. The few normal tissues that tested positive for STOP-1 mRNA showed expression in the stromal tissue, with the exception of the thyroid tissue, which expressed STOP-1 mRNA in its epithelial cells. "-" indicates that the tissues were not examined.

Example 4 - - Northern analysis of STOP-1 mRNA in normal tissues

Human and mouse STOP-1 cDNA probes (full length coding sequences) were radiolabeled with the random-prime kit (Perkin-Elmer) and applied for analysis of human multiple tissue and mouse embryo blots (Clontech) according to the instructions of the manufacturer. The results can be seen in FIG.3a and b.

In normal adult human tissues, the highest STOP-1 mRNA expression was detected in placenta, heart and skeletal muscle (FIG.3a). FIG.3b shows a northern blot that indicates that strong STOP-1 mRNA expression in mouse embryos at 7, 11, 15 and 17 days of development.

Example 5 -- STOP-1 DNA constructs

(a) Mammalian cell expression

All wild type and mutant human, mouse and zebrafish STOP-1 cDNA sequences were made by PCR and expressed in pIRESpuro2 vector (BD Biosiences) or pIRESpuro2 with synthetic 8 X HIS tag coding sequence (HIP) for expression in mammalian cells. Human FAP cDNA were expressed in N-terminal pFLAG-CMV vecor (Sigma).

TABLE 8

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
HIP	GATCGCGGCCG CACACCACCAT CACCATCACCA TCACTAAGTGA (SEQ ID NO:27)	GGCCTCACTTAG TGATGGTGATGG TGATGGTGGTGT GCGGCCGC (SEQ ID NO:28)	BamHI/NotI	pIRESpuro2; HIP – modified original vector with C-terminal HIS, these are 2 adapter oligos
zf762HIP zebrafish construct	CTGCGCTAGCA CCATGATGGGT ACTAAACTGAC	GGAAGCGGCCGC TTTTGGAAGCTCT TCAATGATCA	NheI/NotI	

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
	TCAACTTT (SEQ ID NO:29)	(SEQ ID NO:30)		
m762pIRESpuro2	GAAGCTAGCAC CATGCACCCCC AAGGCCGCGCG GCCCCCCCGCA GCTGCTGCTCG (SEQ ID NO:31)	GAAGCGGCCGCT TATTTCGGTAGTT CTTCAATGATGA T (SEQ ID NO:32)	NheI/NotI	pIRESpuro2
h762pIRESpuro2	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	CAAGCGGCCGCT TATTTTGGTAGTT CTTCAATAATGA T (SEQ ID NO:34)	NheI/NotI	pIRESpuro2
h762HIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	NheI/NotI	HIP
ΔTHDh762HIP (1-54, 94-243, plus His)	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	TCAAAGCTTTCC CTCAGCATTCCA TTATACAGGTCC ACCACCT (SEQ ID NO:36)	NheI/HindIII	h762HIP
ΔΔTHDh762HIP (1-51, 94-243, plus His)	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	CTCAAAGCTTTC CCTCAGATACAG GTCCACCACCTC CCTCTG (SEQ ID NO:37)	NheI/HindIII	h762HIP

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
del-N-ter-HIP (1-32, 54-243, plus His)	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	GGGGAGCTCAGA GGCGCTCGACGG CGCGGGCA (SEQ ID NO:38)	NheI/SacI	HIP
	GAAGAGCTCAG GGAAAGCTTTG AGGAGTCCTGG A (SEQ ID NO:40)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	SacI/NotI	
h762G53AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	ACAGGTCGACCA CCTCCCTCTGCCG GAGCT (SEQ ID NO:39)	NheI/SalI	HIP
	GTGGTCGACCT GTATAATGCAA TGTGCTTACAA GGGCCAGCAGG A (SEQ ID NO:41)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	SalI/NotI	
h762N186AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	AATTGTCGACGC CATTTCAGGGCT TCCTTGGTCCAA (SEQ ID NO:42)	NheI/SalI	HIP
	TGGCGTCGACA ATTAATATTCA TCGCACTT (SEQ ID NO:43	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	SalI/NotI	

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
h762C55AHIP	CCAGCTAGCACCATGCGACCCCAGGGCCCCGCCGCCT (SEQ ID NO:33)	ACAGGTCGACCACCTCCCTCTGCCGGAGCT (SEQ ID NO:39)	NheI/SalI	HIP
	GTGGTCGACCTGTATAATGGAATGGCCTTACAAGGGCCAGCAGGAGTGCCT (SEQ ID NO:44	CAAGCGGCCGCTTTTGGTAGTTCTTCAATAATGAT (SEQ ID NO:35)	SalI/NotI	
h762C93AHIP	CCAGCTAGCACCATGCGACCCCAGGGCCCCGCCGCCT (SEQ ID NO:33)	CTCAAAGCTTTCCCTCAGAGCTTCCCCCTTTTCTCCTTTGAAT (SEQ ID NO:45	NheI/HindIII	h762HIP
h762C109AHIP	CCAGCTAGCACCATGCGACCCCAGGGCCCCGCCGCCT (SEQ ID NO:33)	CCATGAGGCCTGCTTGTAGTTGGGTGTC (SEQ ID NO:46	NheI/StuI	HIP
	AGCAGGCCTCATGGAGTTCATTGAATTAT (SEQ ID NO:47	CAAGCGGCCGCTTTTGGTAGTTCTTCAATAATGAT (SEQ ID NO:35)	StuI/NotIs	
h762C126AHIP	CCAGCTAGCACCATGCGACCCCAGGGCCCCGCCGCCT (SEQ ID NO:33)	TAAACGTTGCCTCCGCAATTTTCCCAAG (SEQ ID NO:48	NheI/AclI	HIP

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
	GGCAACGTTTA CAAAGATGCGT TCAAA (SEQ ID NO:49	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	AclI /NotI	
h762C149AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	GCATGCATTTCT GGCTTTTAGCCG AAGTGAGCCA (SEQ ID NO:50	NheI/NsiI	h762HIP
h762C153AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	CTGGCATGCTGC ATTTCTGCATTTT A (SEQ ID NO:51	NheI/SphI	HIP
	GCAGCATGCCA GCGTTGGTATT TCACATTCAA (SEQ ID NO:52	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	SphI /NotI	
h762C154AHIP	AATGCATGCGC TCAGCGTTGGT ATTTCACA (SEQ ID NO:53	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	NsiI /NotI	h762HIP
h762C166AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	CCTGAGGCCTCA GCTCCATTGAAT GTGAAA (SEQ ID NO:54	NheI/StuI	HIP
	CTGAGGCCTCA GGACCTCTTCC CATTGAA (SEQ ID NO:55	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	StuI/NotI	

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
h762C201AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	TCCGGCGCCAAT TCCTTCAGCAAG TCCTTCCACAGA AGAAGTGCGATG AA (SEQ ID NO:56)	NheI/KasI	HIP
	ATTGGCGCCGG ATTAGTGGATG TTGCTATCT (SEQ ID NO:57	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	KasI /NotI	
h762C218AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	TGAAGCGGTACC AACCCAGATAGC AACATC (SEQ ID NO:58	NheI/KpnI	HIP
	GGCGGTACCGC TTCAGATTACC CAAAAGGAGA (SEQ ID NO:59)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	KpnI /NotI	
h762N52AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	ACAGGTCGACCA CCTCCCTCTGCCG GAGCT (SEQ ID NO:39)	NheI/SalI	HIP
	GTGGTCGACCT GTATGCTGGAA TGTGCTTACAA GGGCCAGCA (SEQ ID NO:60)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	SalI /NotI	

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
h762G53AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	ACAGGTCGACCA CCTCCCTCTGCCG GAGCT (SEQ ID NO:39) Same as for **h762N52AHIP**	NheI/SalI	HIP
	GTGGTCGACCT GTATAATGCAA TGTGCTTACAA GGGCCAGCAGG A (SEQ ID NO:41)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	SalI /NotI	
h762M54AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	ACAGGTCGACCA CCTCCCTCTGCCG GAGCT (SEQ ID NO:39) Same as for **h762N52AHIP**	NheI/ SalI	HIP
	GTGGTCGACCT GTATAATGGAG CGTGCTTACAA GGGCCAGCAGG AGT (SEQ ID NO:61)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	SalI /NotI	
h762P63A, P69AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	TCGGCCGGCCAC TCCTGCTGGCCCT TGTAA (SEQ ID NO:62)	NheI/ NgoMIV	HIP

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
	GTGGCCGGCCG AGACGGGAGCG CTGGGGCCAAT GGCATTCCGGG TA (SEQ ID NO:63	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	NgoMIV/NotI	
h762P75A, P78A, P81AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	TGTGCCGGCAAT GCCATTGGCCCC AGG (SEQ ID NO:64	NheI/ NgoMIV	HIP
	ATTGCCGGCAC AGCTGGGATCG CAGGTCGGGAT GGATTCAAAGG AGAAAA (SEQ ID NO:65)	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	NgoMIV/NotI	
h762K87A, K90AHIP	CCAGCTAGCAC CATGCGACCCC AGGGCCCCGCC GCCT (SEQ ID NO:33)	TTCGCCGGCGAA TCCATCCCGACC TGGGAT (SEQ ID NO:66)	NheI/ NgoMIV	HIP
	TTCGCCGGCGA AGCGGGGGAAT GTCTGAGGGAA AGCTTT (SEQ ID NO:67	CAAGCGGCCGCT TTTGGTAGTTCTT CAATAATGAT (SEQ ID NO:35)	NgoMIV/NotI	
M762HIP	GAAGCTAGCAC CATGCACCCCC AAGGCCGCGCG GCCCCCCCGCA	GAAGCGGCCGCT TTCGGTAGTTCTT CAATGAT (SEQ ID NO:68)	NheI/NotI	HIP

Construct	Forward primer, 5'-3'	Reverse primer, 5'-3'	5'/3' cloning sites	Cloning vector/ comments
	GCTGCTGCTCG (SEQ ID NO:31)			
hFAPCMV	GAAGCGGCCGC AAGACTTGGGT AAAAATCGTAT TT (SEQ ID NO:69)	GAAAGATCTCTA GTCTGACAAAGA GAAACACTGCTT TAGGA (SEQ ID NO:70)	NotI/BglII	N-TER-PfLAG cmv

(b) Baculovirus expression

For expression in baculovirus, the following human STOP-1 constructs were made: S31humanSTOP-1-pAcGP67B encoding S31-K243, L94humanSTOP-1-pAcGP67B encoding L94-K243, and E89humanSTOP-1-pAcGP67B encoding E89-K243 of human STOP-1. S31humanSTOP-1-pAcGP67B was generated in a two step PCR approach. The 5' piece was generated from pAcGP67B using primers #161344 (GGATCGTCGGTTTTGTACAATATGT) (SEQ ID NO:71) and #161347 (GGGGATCTCAGACGCAAAGGCAGAATGCGC) (SEQ ID NO:72). The 3' piece was generated from DNA #84694 using primers #161348 (TCTGCCTTTGCGTCTGAGATCCCCAAGGGG) (SEQ ID NO:73) and #161732 (CCGTTCTGCAGTTAATGATGATGATGATGATGATGATGG) (SEQ ID NO:74). The full length insert (which is then subcloned into pAcGP67B) was generated from a PCR reaction of equal parts 5' and 3' pieces using primers #161344 and #161732.

L94humanSTOP-1-pAcGP67B was generated in a two step PCR approach. The 5' piece was generated from pAcGP67B using primers #161344 and #161349 (GCTTTCCCTCAGCGCAAAGGCAGAATGCGC) (SEQ ID NO:75). The 3' piece was generated from DNA #84694 using primers #161350 (TCTGCCTTTGCGCTGAGGGAAAGCTTTGAGG) (SEQ ID NO:76) and #161346 (CCGGGATCCTTAATGATGATGATGATGATGAT) (SEQ ID NO:77). The full length insert (which is then subcloned into pAcGP67B) was generated from a PCR reaction of equal parts 5' and 3' pieces using primers #161344 and #161346.

DNA #84694 was amplified by PCR to generate two fragments containing S31-K243 and L94-K243 with C-terminal His tags. PCR fragments were subcloned into the baculovirus transfer vector pAcGP67B (PharMingen), which was then co-transfected with BaculoGold DNA (PharMingen) into Sf9 cells. Recombinant virus was isolated and amplified in Sf9 cells.

E89humanSTOP-1-pAcGP67B was generated in a two step PCR approach. The 5' piece was generated from pAcGP67B using primers #161344 (GGATCGTCGGTTTTGTACAATATGT) (SEQ ID NO:71) and #161351 (ATTCCCCCTTTTCCGCAAAGGCAGAATGCGC) (SEQ ID NO:78). The 3' piece was generated from DNA #84694 using primers #161352 (TCTGCCTTTGCGGAAAAGGGGGAATGTCTGAG) (SEQ ID NO:79) and #161346 (CCGGGATCCTTAATGATGATGATGATGATGAT) (SEQ ID NO:77). The full length insert (which is then subcloned into pAcGP67B) was generated from a PCR reaction of equal parts 5' and 3' pieces using primers #161344 and #161346.

Example 6 - - Expression from STOP-1 DNA constructs and purification of proteins

DNA encoding STOP-1 DNA constructs were transfected into CHO-DP12 cells, CHO-psgb cells (hamster galactosyltransferase I deficient epithelial pgsB-618 CHO cells) (ATCC# CRL-2241) or 293 cells (Roche) using calcium phosphate or fugene 6 transfection reagent according to the instructions of the manufacturer (Roche). The growth medias were supplemented with 1mM NiCl, 5mM CaCl2 and 50mM Tris pH 7.6-8.0. Sixteen hours post transfection the serum containing the media was replaced with serum free media and protein was allowed to accumulate for 4-6 days. The secreted proteins were purified using Ni-NTA agarose beads.

Proteins from cell lysates were prepared by lysing the cells four days after transfection in buffer containing 50 mM HEPES (pH 7.5), 150 mM NaCl, 1% Triton X-100, 5 mM EDTA, 1 X protease inhibitor cocktail (ROCHE, [lysis buffer]). Immunoprecipitation was performed by preclearing cell lysates (2 hr at 4°C) with 25 μl of immobilized protein A/G- agarose beads (Pierce) followed by incubation (4 hr at 4°C) of aliquots (0.5 ml) of lysates (4×10^5 cells per aliquot) with anti-HIS epitope antibody (Qiagen) and with protein A/G–agarose beads. Immunoprecipitates were washed three times with lysis buffer and once with phosphate-buffered saline, fractionated by 10% SDS–PAGE, and transferred to a

nitrocellulose membrane (Invitrogen). Western blot analysis was performed with mouse anti-HIS and the ECL kit (Amersham).

FIG.4a shows that CHO-DP12 cells, used routinely for expression of recombinant proteins, produced little secreted STOP-1. In contrast, a CHO mutant cell deficient in proteoglycan synthesis, CHO-Psgb, produced much more secreted STOP-1 and yielded a better recovery of the secreted proteins in soluble form (FIG.4b). pRK5 was transfected as a negative control. FIGs.5a and b show that His-tagged protein can be detected with anti-His antibodies in cell supernatants and in cell lysates, respectively, of CHO-psgB transfected cells.

For protein production from baculovirus, Hi5 cells were infected with amplified baculovirus. After 3 days in culture at 27°C, the medium was harvested by centrifugation. The supernatant was supplemented with 50mM Tris 8.0, 1mM $NiCl_2$, 5mM $CaCl_2$, and the pH was adjusted to 7.6. The medium was filtered and loaded onto a Ni-NTA agarose column (Qiagen). The column was washed with 50mM Tris 8.0, 300mM NaCl, 2mM benzamidine, 0.5mM PMSF, and 5mM imidazole. Elution was performed in the same buffer with 300mM imidazole. Fractions containing STOP-1 were pooled and concentrated. Protein was purified over a Superdex-75 column into 50mM Tris 8.0, 100mM NaCl, 0.5mM PMSF, and 2mM benzamidine. STOP-1 containing fractions were pooled, concentrated, and utilized for crystallography trials and other studies.

Example 7 - - STOP-1 oligomerization

Full length STOP-1-HIS proteins or various truncations thereof were expressed in SF9 baculovirus-infected cells or CHO cells as described above. The proteins were purified from the media by using Ni-NTA agarose beads as discussed above. The baculoviral-expressed proteins S31-K243-His, E89-K243-His, or L94-K243-His were loaded onto an 8mm x 300mm Shodex KW802.5 size exclusion column and eluted with 100mM NH_4HCO_3, 200mM NH_4Cl pH7.8 at a flow rate of 1ml/ml. CHO-psgb expressed full length proteins were loaded onto an 8mm x 300mm Shodex KW804 size exclusion column and eluted with 25 mM sodium phosphate, 500mM NaCl at a flow rate of 1ml/ml. CHO-psgb expressed proteins, M1-M54 fused to L94-K243-His, were loaded onto an 8mm x 300mm Shodex KW802.5 size exclusion column and eluted with 25 mM sodium phosphate, 500mM NaCl at a flow rate of 1ml/ml.

The eluted protein was analyzed by an Agilent Model 1100 HPLC system with an Agilent multi wavelength detector (UV) connected to a Wyatt MiniDAWN laser light scattering (LS) instrument and a Wyatt Optilab differential refractometer (RI). The average molecular weight of the proteins or their aggregates in each peak was determined by selecting a peak and using the Zimm fitting method (Phillip J. Wyatt , (1993) Analytica Chimica Acta 272:1-40) with the Astra software package (Wyatt, USA). The percentage of aggregation was calculated from the integrated peak areas of the UV signal at 214 nm. See FIG.6 and FIG.7 for results.

Light scatter analysis indicates that the baculovirus S31-K243-His proteins primarily formed trimeric molecules (apparent molecular weight 74kD, 95% of total integrated peak area) (FIG.6A). The baculovirus E89-K243-His proteins formed complexes that were approximately 36% trimeric and 64% hexameric (i.e., apparent MW of 126kD representing 36% of peak area, apparent MW of 61kD representing 64% of peak area) (FIG.6B). However, it is believed that the hexameric complexes formed by E89-K243-His are an anomaly due its odd number of cysteines. The baculovirus L94-243 protein, which lacks the triple helix domain, forms trimeric complexes (apparent MW of 59kD representing 98% of peak area) (FIG.6C). This indicates that the N-terminal domain of the protein and the triple helix domain are not required for trimerization. The L94-K243 region is sufficient. The THD can act to stabilize the trimers.

Proteins expressed in CHO-psgb also formed complexes (FIG.7A-C). Light scatter analysis indicated that the full length-expressed protein (M1-K243-His) formed complexes that were approximately 58% hexameric and 42% trimeric (FIG.7A). The complexes formed by delta-THD expression (M1-M54 and L94-L243-His) were in part trimeric (apparent MW of 66kD representing 61% of peak area) and in part heterogeneous in mass (average MW of 627kD) probably due to the varied glycosylation state of the proteins in CHO cells (FIG.7B).

On SDS gels, purified full-length STOP-1 expressed in CHO-psgB cells migrated as a monomer under reducing conditions and as a dimer under non-reducing conditions (without DTT). See FIG.7C. The results indicate that disulfide bonding can occur between two monomers.

<u>Example 8 - - Deletion and Point Mutational Analysis of STOP-1</u>

Full-length STOP-1 (WT)-His, delta-THD-His, delta-delta-THD-His, delta-N-terminus and several point mutation mutants were expressed in CHO-psgb cells as described above. Whole cell extract extracts were prepared. Aliquots from the whole cell extracts or

the media in which the cells were cultured were run on an SDS gel under reducing and non-reducing conditions and western blotted with anti-His antibody (ECL detection kit, Amersham).

FIG.8A and B indicates that a disulfide bond can form between two monomers in the THD region in extracts from supernatants and lysates, respectively. Each deletion mutants lacking the THD, which includes cysteine 55 failed to form dimers under non-reducing conditions. Homodimers were present in the supernatant and lysates of cells expressing full length protein under non-reducing conditions, but not under reducing conditions. Table 9 summarizes the results as follows:

TABLE 9

Construct	Secretion	Dimerization
WT	+	+
delta-THD	+	-
delta-delta-THD	+	-
delta-N-ter	+	+

"+" indicates that the level of secretion or dimerization was the same as wild-type STOP-1.
"-" indicates that dimerization was not detectable in this assay.

Point mutants of human STOP-1 were tested for the ability to secrete and dimerize. FIG.9A and B shows that wild-type STOP-1 protein and a G53A mutant were secreted and that homodimers are observed in the in supernatants and lysates. However, a mutant at 186 ("N" mutated to "A"), a potential glycosylation site, was not present in the culture media and did not homodimerize. Many other mutants were also tested. Table 10 summarizes the results as follows:

TABLE 10

Construct	Secretion	Dimerization
WT	+	+
N52A	+	+
G53A	++	+
M54A	+	+

P63A, P69A	+	+
P75A, P78A, P81A	+	+
K87A, K90A	+	+
N186A	-	-

"+" indicates that the level of secretion or dimerization was the same or better ("++") than wild-type STOP-1. "-" indicates that secretion or dimerization was not detectable in this assay. All these mutants except N186A were secreted and ran similar to WT on SDS gels.

FIG.10A and B show the state of the a human STOP-1 protein having point mutations at cysteine residues 55, 93 and 109. Point mutations were also made at other cysteines throughout the protein. Table 11 summarizes the results as follows:

TABLE 11

Construct	Secretion	Dimerization
WT	+	+
C55A	+	-
C93A	+	+
C109A	-	
C126A	-	
C153A	-	
C154A	-	
C153A, C154A	-/+	-/+
C166A	-	
C201A	-	
C218A	-	

"+" indicates that the level of secretion or dimerization was the same as wild-type STOP-1. "-" indicates that dimerization was not visibly detectable in this assay. "-/+" indicates that secretion or dimerization was weakly detectable in this assay.

All of the mutants were expressed, but only two were secreted - - C55A and C93A. C93A was secreted and formed dimers in contrast to C55A, which was secreted but did not form dimers indicating that C55 is required for intra-subunit disufide bonding.

Example 9 - - Wnt pathway upregulates STOP-1 mRNA

The STOP-1 gene is located on human chromosome 8 between 8q22 and 8q23. The gene is located close to genes encoding proteins important in the Wnt signalling pathway such as the FZD6 gene (frizzled homolog 8 (drosophila)), the WISP-1 gene (WNT1 inducible secreted protein 1). There are at least three regulatory genes in the Wnt pathway that are mutated in primary human cancers and experimental tumors of other species.

MMTV-Wnt-1 transgenic mice were prepared by Genentech, Inc. These mice overexpress the Wnt-1 protein under the control of the MMTV promoter. The C57Mg cells do not overexpress Wnt-1. Breast tumors in these mice were removed. mRNA was extracted from the breast tumors or from C57Mg mammary epithelial cells. A reverse transcriptase reaction was performed with an oligo(dT) primer, the avian myeloblastosis virus reverse transcriptase (Promega) and the extracted mRNA according to manufacturer's instructions (Promega). PCR on the reverse transcribed products was carried out with Ex-taq polymerase (Takara) using mRLP19 primers and mouse STOP-1 primers:

mRPL19:
5'-ATCGCCAATGCCAACTCCCGTCA-3' (SEQ ID NO:80) and
5'-GCTTGCGTGCTTCCTTGGTCTTA-3' (SEQ ID NO:81).

mRLP19 is the murine mitochondrial ribosomal protein L19 (MRPL19), a housekeeping protein. PCR using primers against mRLP19 was used as a control for the extraction and PCR of mRNA.

mSTOP-1:

5-TGCTGCTGCAGCTGCCCGCGCCGTCGAG-3 (SEQ ID NO:82) and
5-TCCAGTAGAAGCATCTCCTTTTGGGTAA-3 (SEQ ID NO:83).

The results show that mSTOP-1 mRNA is expressed in the breast tumors of MMTV-Wnt-1 transgenic mice (FIG.11, lanes T1-T7), whereas it is not expressed in C57Mg normal mouse mammary epithelial cells ("N"). Thus, a connection is suggested between the Wnt signalling pathway and STOP-1 expression.

Example 10 - Coexpression of STOP-1 with other genes

A proprietary database containing gene expression information (GeneExpress®, GeneLogic Inc., Gaithersburg, MD) was analyzed for genes that are expressed in the same tissues as STOP-1 (BLIST analysis, proprietary software written an developed at Genentech, Inc. for use with the GeneExpress® database). By this method, several genes having significant correlation of expression in breast and colon tumors were identified. Genes that were coexpressed in breast and colon tumors included, Wisp-1 (a WNT target gene), SFRP2 (a soluble WNT receptor), fibroblast activation protein (FAP), a cell surface serine protease that has been implicated in ion cancer), collagen type I alpha 2 chain, collagen type V alpha 2 chain, Thrombospondin 2 (THBS2) (ECM), ADAM12 (a MMP enzyme), OB-Cadherin and OSF-2 (TCI protein). The later genes suggest involvement of STOP-1 in formation and/or modulation of the extracellular matrix.

Example 11 - STOP-1 is cleaved by MMP-7 and MMP-9 in vitro

Materials: Human his-tagged STOP-1 protein was produced using a baculovirus expression system. Matrix metalloproteases (MMPs)-1, -2, -3, -7, and -9 were purchased from Enzyme Systems Products. Trypsin was obtained from Sigma.

Proteolytic Digestion of STOP-1: Prior to reaction with STOP-1, MMPs were activated with 1 mM p-aminomercuric acetate for 1h at 37 degrees Celsius. STOP-1 (3 μg) was digested with proteases (50 or 250 nM) in a final volume of 20 μl for 4 hours at 37 degrees Celsius. Buffer A (50 mM Tris, pH 87.5, 10 mM $CaCl_2$, 10 μM $ZnCl_2$ and 100 mM NaCl) was the buffer used for the MMP cleavage reaction. Buffer A lacking $ZnCl_2$ was the buffer used for the trypsin cleavage reactions. The MMP reactions were terminated by addition of EDTA (15 mM). The trypsin reaction was terminated by addition of PMSF (1 mM). Samples were then analyzed by SDS-PAGE and Coomassie staining.

FIG.23 shows the cleavage of baculoviral expressed human STOP-1 protein by various proteases *in vitro*. MMP-7 also cleaved human STOP-1 *in vitro*, whereas MMP-1, -2 and –3 produced minimal or no cleavage products (data not shown). MMP-7 produced STOP-1 cleavage products of about 23 and 21 kDa. In contrast, MMP-9 produced STOP-1 cleavage products of about 22 and 18 kDa. Tyrpsin produced 20 and 22 kDa fragments (data not shown). These data suggest that STOP-1 activity may be regulated by proteolysis. This

can be particularly relevant with tumor stromal-associated proteases such as MMP-7 and MMP-9.

Example 12 - STOP-1 expression promotes 3T3 proliferation

(a) Cell culture and generation of 3T3 STOP-1 stable cell lines

3T3 cells were maintained in DMEM supplemented with 10% FCS. Mouse and human STOP-1-expressing cell lines were established by transfection of 3T3 cells with m762pIRESpuro2 and h762pIRESpuro2 vectors using FuGENE 6 transfection reagent (Roche) according to the instructions of the manufacturer. STOP-1 clones were established by selecting transfected cells with puromycin (4g/ml).

(b) *In vitro* proliferation assay

3T3 cells were transfected with mouse STOP-1, human STOP-1 or vector alone as described above and were plated in 96-well plates at $1.5x10^3$ cells in DMEM with 10% FCS. Twelve hours later the media was change to DMEM with 1.5% FCS and 10uCi/ml [^{3}H]-thymidine. After 12 hours, 48 hours and 96 hours, the cells were harvested onto a GF/C filter using Packard's 96-well Filtermate 196, washed and counted on a top count, microplate scintillation counter (Packard). The results show that clones expressing STOP-1 demonstrated increased proliferation as compared with vector alone-transfected clones (puro2 and ph1). See FIG.12A and B.

(c) Retroviral expression in 3T3 cell lines

A human full-length STOP-1 cDNA was cloned from H762pirespuro2 into the pMSCV1(puro) vector (Clontech) and introduced into 3T3 fibroblasts and 293 cells by retroviral infection using the method described by Maecker et al., (Maeker H.L., et al., Cancer Cell 2, 139-148, 2002). Briefly, 5000 cells/well were plated in 96 well plates and switched to low serum media (0.25% fetal calf serum) the following day. The retrovirally infected cells were selected in puromycin (3 ug/ml). After 24 hours, cell proliferation was measured using the Cell Titer Kit (Promega). FIG.13C shows that infection with STOP-1 retrovirus promotes proliferation of both 3T3 and 293 cells, respectively, as compared to 3T3 or 293 cells infected with a control.

For detection of STOP-1 protein, whole cell lysates of cell pellets (~ 2 x 10^6 cells) were prepared and incubated with antibody S7-IgG (1 μg) described below and subsequently immunoprecipitated with protein A/G. Immunoprecipitates were then denatured and transferred to nitrocellulose membranes. STOP-1 was then detected using rabbit polyclonal anti-STOP-1 antibodies. FIG.13A and B show expression of STOP-1 in 3T3 and 293 cells in whole cell lysates following infection with STOP-1 retrovirus as compared to a vector control, Babe.

Example 13 - STOP-1 expression causes tumorigenesis in mice

Female athymic nu/nu mice (Charles River Laboratory, [5 animals per group]) were inoculated subcutaneously with 1x10^6 3T3 cells stably transfected with mouse or human STOP-1, RAS cDNA (Hudziak RM, Lewis GD, Shalaby MR, Eessalu TE, Aggarwal BB, Ullrich A, Shepard HM. (1988) Proc Natl Acad Sci. 85(14), pp.:5102-6) or an empty puro2 vector (p2). Tumor growth was measured 1 time per week. The stably 3T3 cell lines were also evaluated for STOP-1 expression by preparing whole cell lysates of pelleted cells, performing SDS-PAGE on aliquots of the lysates or cell culture media, and western blotting the gels and probing them with rabbit anti-STOP-1 antibody. Cells transfected with RAS cDNA served as positive controls. See FIG.14A-C.

The results show that murine STOP-1 was present in the lysates of all of the NIH 3T3 clones, but was only present in the cell culture media of two of the three NIH 3T3 clones (FIG.14B and C, respectively). In other words, clone 18 expressed the protein intracellularly but was defective at secreting the murine STOP-1 protein. See FIG.14B. Further, the two clones that secreted STOP-1 produced tumors in nude mice whereas the clone that was deficient in secretion did not (FIG.14A). These results suggest that secreted murine STOP-1 by itself can be tumorigenic whereas intracellularly expressed STOP-1 is not.

The results also show that human STOP-1 can drive tumorigenesis in mice. See FIG.15. Tumors grew in several mice that expressed the human STOP-1 protein and in the RAS control, but not in the mice treated with cells transfected with vector alone. Like the mouse STOP-1, these results suggest that secreted human STOP-1 by itself can be tumorigenic.

Example 14 - STOP-1 Promotes Wound Healing

Malignant melanoma SK-MEL-31 cells were maintained in DMEM supplemented with 10% FCS. SK-Mel-31 cells were cultured in 6 well dishes (Corning) until they reached subconfluency, then starved for 8 hours in DMEM with 2% heat-inactivated FCS. The cells were then treated for 2 hours in FCS-free DMEM with 10 μg/ml mitomycin C (Sigma) and subjected to the following *in vitro* wound closure assay.

A cell-free area was introduced by scraping the SK-MEL-31 cell monolayer with a yellow pipette tip. Cell migration to the cell-free area for 48 hours after scraping was evaluated while the cells were maintained in DMEM supplemented with 2% heat-inactivated FCS in the absence or presence of 30 ng/ml EGF (Roche), 1 g/ml of full length baculovirus expressed human STOP-1 protein, both or none. FIGs.16A-E are phase-contrast photographs of the scraped area 48 hours after scraping.

The results show that cells migrated to the scraped area when treated with EGF or STOP-1, especially STOP-1 expressed from CHO-psgB cells. The results indicate that STOP-1 promotes cell migration. Cell migration occurs in tumor growth as it invades surrounding tissue. The data further supports the tumor promoting properties of STOP-1.

Example 15 - Monoclonal antibody development

Ten BALB/c mice (Charles River Laboratories, Wilmington, DE) were hyperimmunized with recombinant polyhistidine-tagged (HIS8) human STOP-1 (a.k.a. DNA 145960) transiently expressed in PSGB chinese hamster ovary cells (Genentech, Inc., South San Francisco, CA) in Ribi adjuvant (Ribi Immunochem Research, Inc., Hamilton, MO). B-cells from five mice demonstrating anti-STOP-1 antibody titers were fused with mouse myeloma cells (X63.Ag8.653; American Type Culture Collection, Rockville, MD) using a modified protocol analogous to one previously described (Kohler, G. and Milstein, C. (1975) Nature 256: 495-497; Hongo, J.S., et al., (1995) Hybridoma 14:253-260).

After 10-14 days, the supernatants were harvested and screened for antibody production by direct enzyme-linked immunosorbent assay (ELISA). One positive clone (6B12.1.7), showing the highest immunobinding after the second round of subcloning by limiting dilution, was injected into Pristane-primed mice (Freund YR and Blair PB (1982) J Immunol 129:2826-2830) for *in vivo* production of MAb. The ascites fluid was pooled and purified by Protein A affinity chromatography (Pharmacia fast protein liquid chromatography [FPLC]; Pharmacia, Uppsala, Sweden) as previously described (Hongo et al., 1995, supra).

The purified antibody preparation was sterile filtered (0.2-µm pore size; Nalgene, Rochester NY) and stored at 4°C in phosphate buffered saline (PBS). The hybridoma clone producing the 6B12 antibody was deposited under the terms of the Budapest Treaty with the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209, USA on March 28, 2003 as "6B12.1.7".

The binding site for the 6B12 antibody was mapped to an N-terminal region of human STOP-1. The His-tagged constructs encoding the human full length protein, the delta-THD protein, the delta-delta-THD protein, the delta-N-terminal protein and the zebrafish full length protein were expressed in CHO-psgB cells. Aliquots of transfected cell extracts were run on SDS-PAGE, western blotted and probed with either anti-His antibody or 6B12 antibody.

The 6B12 monoclonal antibody worked well on westerns. See FIG.17C. It bound to all of the human proteins expressed as described above except for the delta-N-terminal protein. Therefore, the binding epitope of the 6B12 antibody maps to the N-terminal amino acids #33-52 of human STOP-1. The 6B12 antibody did not recognize the zebrafish STOP-1 protein on a western blot.

Example 16 - Phage-derived antibodies against STOP-1

Overview: Phage-derived antibodies against STOP-1 were made using, in part, materials and methods described in United States Provisional Application No. 60/385,338 ("the '338 application"), filed June 3, 2002. In this study, phagemids were further modified and the resultant antibodies were screened based on binding to oligomerized STOP-1.

Construction of Anti-Her2 Fab and F(ab)'$_2$ phagemid: The phagemid vector, pS0643 (also known as phGHam-g3, e.g., United States Patent 5,688,666, Example 8), contains pBR322 and f1 origins of replication, an ampicillin resistant gene, an E. coli alkaline phosphatase (phoA) promoter (Bass et al., (1990) *Proteins* 8:309-314), and a sequence encoding a stII secretion signal sequence fused to residues 1-191 of human growth hormone (hGH) and a sequence encoding the C-terminal residues 267-421 of protein III of M13 phage (hereinafter, cP3). The pS0643 phagemid also contains an XbaI site and an amber stop codon following residue 191 of hGH. The stII secretion signal sequence can export a protein to the periplasm of a bacteria cell (e.g., a light chain region (LC) of an antibody). In this study, the sequence encoding the human growth hormone (hGH) was removed from the pS0643 vector and replaced with a NsiI/XbaI nucleic acid fragment encoding a humanized anti-Her2 Fab

fragment ("h4D5" sequence) ligated in frame with the stII secretion signal (humAb4D5-8, *see* Carter et al., (1992) PNAS 89:4285-4289, Table 1 and FIG.1 therein or U.S. Patent No. 5,821,337, for sequence).

The h4D5 antibody is a humanized antibody that specifically recognizes a cancer-associated antigen known as Her-2 (erbB2). In this study, the h4d5 was obtained by polymerase chain reaction using the humAb4D5 version 8 ("humAb4D5-8") sequence and primers engineered to give rise to a 5' NsiI site and a 3' XbaI site in the PCR product (Carter et al., (1992) PNAS 89:4285-4289). The PCR product was cleaved with NsiI and XbaI and ligated into the pS0643 phagemid vector. The h4D5 nucleic sequence encodes modified CDR regions from a mouse monoclonal antibody specific for Her-2 in a mostly human consensus sequence Fab framework. Specifically, the sequence contains a kappa light chain (LC region) upstream of V_H and C_H1 domains (HC region). The method of making the anti-Her-2 antibody and the identity of the variable domain sequences are provided in U.S. Pat. Nos. 5,821,337 and 6,054,297.

The pS0643 plasmid containing humanized 4D5 (version 8) was still further modified. For example, a herpes simplex virus type 1 glycoprotein D epitope tag (gD tag) was added in frame to the c-terminus of the LC using site-directed mutagenesis. Following the stop codon downstream of the LC, a ribosome binding site and nuclec acid molecule encoding a stII signal sequence were ligated to the N-terminus of the HC sequence. Consequently, the HC sequence is in frame with the C-terminal domain of the p3 (cP3), a minor coat protein of M13 phage. Thus, a Fab displayed on phage can be produced from one construct. This Fab phagemid vector is referred to as pV0350-2b (FIGs.25A-H) and can be schematically illustrated as FIG.24A.

To generate F(ab)'$_2$ displayed on phage, the PV0350-4 vector was further modified by inserting a dimerizable leucine zipper GCN4 sequence (GRMKQLEDKVEELLSKNYHLENEVARLKKLVGERG) (SEQ ID NO:84) between the HC and cP3 sequences by cassette mutagenesis. The GCN4 leucine zipper brings two sets of LC/HC-cP3 fusion polypeptides together in the *E. coli* periplasm and presents the dimer on the surface of phage. This F(ab)'$_2$ phagemid vector is referred to as pV0350-4 (FIGs.27A-H) and can be schematically illustrated as FIG.24B.

Generating F(ab) Libraries with H1/H2/H3 Diversity for Use in STOP-1 selection:

A diversified library for finding anti-STOP-1 antibodies was created by mutating the sequences encoding the HC variable regions in the pV0350-2b and pV0350-4 vector using

Kunkel mutagenesis and screening the phage containing them based on binding to human STOP-1 by ELISA assay. The screening method is described in greater detail below. Other antibodies having greater specificity or affinity to STOP-1 can be obtained by, e.g., further mutagenizing the Fab and F(ab)'$_2$ sequences (e.g., by Kunkel mutagenesis, (Kunkel et al., (1987) *Methods Enzymol.* 154:367-382)) in their LC CDR regions and screening them by binding to STOP-1.

Expression of phage: E. coli strain SS320 was transformed with the mutagenized DNA described above by electroporation. The size of the libraries was approximately 10^9. Transformed bacterial cells were grown up overnight in the presence of helper phage KO7 to produce displaying phage that could still infect other bacterial cells. Next, *E. coli* strain XL-1 Blue (Strategene, San Diego, CA) was infected with F(ab) or F(ab)'$_2$ phage and then K07 helper phage (Strategene, San Diego, CA) were grown in 2YT media at 37°C for 20 hours and phage was harvested as described (Sidhu et al., Methods Enzymol. (2000), 328:333-363). Briefly, phage was purified by first precipitating them from the overnight culture media with polyethylene glycol, and resuspended in PBS. Phage were quantitated by spectrophotometer with its reading at 268nm (1 OD=1.13 x 10^{13}/ml).

Phage sorting: The phage libraries were subjected to four rounds of sorting. 96-well Nunc Maxisorp plates were coated with 100ul/well of target antigen (CHO-psgb-expressed human his-tagged STOP-1 full length or baculovirally-expressed human his-tagged #94-243 amino acids ("short form")) (5ug/ml) in PBS at 4°C overnight or room temperature for 2 hours. The plates were blocked with 65ul 1% blocking protein for 30min and 40ul 1% Tween20 for another 30min (blocking protein: 1st round – bovine serum albumin (BSA), 2nd round -ovalbumin, 3rd round -casein, 4th round -ovalbumin). Next, the library phage was diluted to 3~5 O.D/ml with 1%BSA with 0.1% Tween 20 (1 O.D=1.13 x 10^{13} phage/ml). In general, the phage input was 1st round 3-5 O.D/ml, 2nd round 3 O.D/ml, 3rd round 0.5~1 O.D/ml and 4th round input 0.1~0.5 O.D/ml. The diluted phage was incubated for 30 minutes at room temperature. The wells were washed at least five times continuously with PBS and 0.05% Tween 20. The blocked library phage was added 100ul/well to 8 target antigen-coated wells and 2 uncoated wells at room temperature for 1hour. The plates were washed continuously at least 10 times with PBS and 0.05% Tween 20. The phages were eluted with 100ul/well of 100mM HCl at room temperature for 20minutes. The eluted phages (from coated wells) and background phage (from uncoated wells) were collected in separate tubes. The eluted collections were neutralized by adding 1/10 volume 1M Tris pH 11.0 to both tubes. BSA was added to a final 0.1% into the tube of eluted phage. The eluted phage was

heated at 62C for 20 minutes. To titer the phage, 90ul of log phase XL-1 (OD 600nm~0.1-0.3) was infected with 10ul eluted phage or background phage at 37°C for 30 minutes. Next, the infected cells were serially diluted in 10 fold increments with 90ul 2YT. 10ul aliquots of the infected cells were plated per carbenicillin plate.

To propagate the phage, approximately 400ul of eluted phage was used to infect ~4ml log phase XL-1soup (OD 600nm~0.1-0.3) at 37°C for 30-45minutes. Helper phage, KO7, and carbenicillin were added to the infection at a final concentration of 1 x 10^{10} pfu/ml KO7and 50ug/ml cabenicillin at 37°C for another hour. The culture was grown in 50:50 2YT/CRAP media with carbenicillin 50ug/ml and 50ug/ml kanamycin to final volumes of 20~25ml at 37°C overnight (or at least 17 hours). The next day, the culture was grown at 30C for another 2 hours to increase the phage yield.

The phage was purified by spinning down the cells at 8000 rpm for 10 minutes. The supernatant was collected. 20% PEG/2.5M NaCl was added at 1/5 of the supernatant volume, mixed and allowed to sit on ice for 5 minutes. The phage was spun down into a pellet at 12000 rpm for 15 minutes. The supernatant was collected and spun again for 5 minutes at 5000 rpm. The pellets were resuspended in 1ml PBS and spun down at 12000 rpm for 15 minutes to clear debris. The steps starting with the PEG/NaCl addition were repeated on the resuspended pellet. The OD of the resupended phage pellet was read at 270nm.

The second, third and fourth rounds of phage sorting were completed by repeating the phage sorting steps as described above. The phage antibodies that were selected based on binding to the short form were designated as "S#" (e.g., S4, S9, S7 and S16). The phage antibodies that were selected based on binding to the full length form were designated as "F#" (e.g., F5, F6, F13 and F47).

ELISA Screening Assay: Clones from the sorts 2 to 4 were screened for specificity and affinity by ELISA assay. Positive clones (binders) were clones that had above background binding to the target antigens and not to other non-relevant protein, such as bovine serum albumin and insulin-like growth factor-1 (IGF-1).

First, the wells of a 384-well microtiter plate were coated with either full length or "short form" (#93aa-243aa) his-tagged human STOP-1, IGF-1, Her-2 or anti-gD at 20ul per well (2µg/ml in PBS) at 4°C overnight or room temperature for 2 hours.

HER2	STOP-1
Anti-gD	IGF-1

In another 96 well plate, colonies from sorts 2-4 were grown overnight at 37°C in 150ul 50:50 2YT/CRAP media with 50ug/ml carbenicillin and helper phage K07. The plate was spun down at 2500 rpm for 20 minutes. 50ul of the supernatant was mixed with 120ul of ELISA buffer (PBS - 0.5% BSA and 0.05% Tween20). 30ul of the mixture was added to each quadrant of the 384-well coating plate and incubated at room temperature for 1 hour. Binding was quantified by adding 75ul/well of horse radish peroxidase (HRP)-conjugated anti-M13 antibody in PBS plus 0.5%BSA and 0.05% Tween20 at room temperature for 30 minutes (Sidhu et al., supra). The wells were washed with PBS - 0.05% Tween20 at least five times. Next, 100ul/well of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) Peroxidase substrate and Peroxidase Solution B (H_2O_2) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) was added to the well and incubated for 5 minutes at room temperature. The reaction was stopped by adding 100ul 1M Phosphoric Acid (H_3PO_4) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) to each well. The OD of the yellow color in each well was determined using a standard ELISA plate reader at 450 nm. The F(ab)or F(ab)'$_2$ phage concentration that resulted in about 90% of maximum binding to the coated plate was used in the solution binding competition ELISAs. F(ab) and F(ab)'$_2$ phage having 3-4 fold greater binding than BSA, IGF-1, Her2 and anti-gD were considered to have better specificity. Those binders were sequenced.

FIG.18 shows a partial amino acid sequence of several of the binders that had higher affinity and specificity (e.g., S7, S16, F5, S9, F13, F47 and S9). Three clones share identical CDR sequences - - F13, F47 and S4. S7 and S16 also share some sequence homology. Based on the sequence homology between F13, F47, S4, S7, S9 and S16 in their V_H-CDR1, V_H-CDR2 and V_H-CDR3 regions, consensus sequences for the commonly recognized epitope were derived. Amino acid and nucleic acid sequences coding for a phage display S4-Fab, a phage display S9-Fab, a phage display S7-F(ab)'2, a phage display S16-F(ab)'2, a phage display F5-F(ab)'2 can be found in FIGs.27A-C, FIGs.28A-C, FIGs.29A-C, FIGs.30A-C and FIGs.31A-C, respectively.

The following vectors have been deposited under the terms of the Budapest Treaty with the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209, USA as described below:

Material	Deposit No.	Deposit Date
V0350-4-S7	PTA-5090	March 25, 2003
V0350-4-S16	PTA-5089	March 25, 2003

V0350-2b-S4	PTA-5086	March 25, 2003
V0350-2b-S9	PTA-5087	March 25, 2003
V0350-4-F5	PTA-5088	March 25, 2003

Example 17 - - Solution Binding Competition ELISA

To determine a binding affinity for selected F(ab) and F(ab)'$_2$ phage, competition ELISAs were performed.

First, the phage were propagated and purified. Ten uls of XL-1 bacteria infected with one of the clones for 30 minutes at 37°C was plated on a carbenicillin plate. A colony was picked and grown in 2 mls (2YT and 50ug/ml carbenicillin) at 37°C for 3-4 hours. Helper phage, KO7, was added to the culture at a final concentration of 10^{10} pfu/ml for another 1 hour at 37°C. Twenty mls of media (2YT/CRAP 50:50 with 50ug/ml carbenicillin was added to the culture for growth overnight at 37°C. The phage was purified as described above.

Second, the concentration of purified phage that would be optimal for use in the following competition ELISA assay was determined (i.e., approximately 90% of maximal binding capacity on the coated plate). 96-well Nunc Maxisorp plates were coated with full length or short form human STOP-1 (2ug/ml in PBS) at 4°C overnight or at room temperature for 2 hours. The wells were blocked by adding 65ul 1% BSA for 30 minutes followed by 40ul 1% Tween20 for another 30 minutes. Next, the wells were washed with PBS - 0.05% Tween20 5 times. Various dilutions of F(ab) or F(ab)'$_2$ phage down to 0.1 O.D./ml in ELISA buffer (PBS - 0.1%BSA and 0.05% Tween20) were added to the wells for 15 minutes at room temperature. The wells were then washed with PBS - 0.05% Tween20 at least three times. 75ul of HRP-conjugated anti-M13 antibody (Amersham, 1/5000 dilution with ELISA buffer) per well was added and incubated at room temperature for 30 minutes. The wells were washed again with PBS - 0.05% Tween20 at least five times. Next, 100ul/well of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) Peroxidase substrate and Peroxidase Solution B (H_2O_2) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) was added to the well and incubated for 5 minutes at room temperature. The reaction was stopped by adding 100ul 1M Phosphoric Acid (H_3PO_4) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) to each well. The optical density of the color in each well was determined using a standard ELISA plate reader at 450 nm. The dilutions of phage were plotted against the O.D. readings.

Third, a competition ELISA was performed. 96-well Nunc Maxisorp plates were coated with full length or short form human STOP-1 (2ug/ml in PBS) at 4°C overnight or at

room temperature for 2 hours. The wells were blocked by adding 65ul 1% BSA for 30 minutes followed by 40ul 1% Tween20 for another 30 minutes. The wells were washed with PBS - 0.05% Tween20 5 times. Based on the binding assay above, 50ul of the dilution of phage that resulted in about 90% of maximum binding to the coated plate was incubated with 50ul of various concentrations of full length or short form human STOP-1 (0.1 to 500nM) in ELISA buffer solution for 1 hour at room temperature in a well. The unbound phage was assayed by transferring 75ul of the well mixture to second 96-well plate pre-coated with full length or short form human STOP-1 and incubating at room temperature for 15 minutes. The wells of the second plate were washed with PBS - 0.5% Tween20 at least three times. 75ul of HRP-conjugated anti-M13 antibody (1/5000 dilution with ELISA buffer) per well was added and incubated at room temperature for 30 minutes. The wells were washed again with PBS - 0.05% Tween20 at least five times. Next, 100ul/well of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) Peroxidase substrate and Peroxidase Solution B (H_2O_2) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) was added to the well and incubated for 5 minutes at room temperature. The reaction was stopped by adding 100ul 1M Phosphoric Acid (H_3PO_4) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) to each well. The optical density of the color in each well was determined using a standard ELISA plate reader at 450 nm. The concentrations of competitor STOP-1 were plotted against the O.D. readings. The IC50, the concentration of STOP-1 that inhibits 50% of the F(ab)-phage or F(ab)'$_2$-phage, represents the affinity. See Table 12.

Table 12 shows that F5 binds the N-terminus of full length STOP-1, not the short form. S7, S16, S9 and S4 (and therefore F13 and F47) bind to the short form (#94-243) of human STOP-1. In Table 2, the term "762 S/S" indicates that the wells of the microtiter plate were coated with the short form of human STOP-1 and that the F(ab)-phage or F(ab)'$_2$-phage were competed with the short form of human STOP-1. The term "762 S/F" indicates that the wells of the microtiter plate were coated with the short form of human STOP-1 and that the F(ab)-phage or F(ab)'$_2$-phage were competed with the full length form of human STOP-1. The term "762 F/F" indicates that the wells of the microtiter plate were coated with the full length form of human STOP-1 and that the F(ab)-phage or F(ab)'$_2$-phage were competed with the full length form of human STOP-1. "ND" indicates that the result was not detectable. "N/A" indicates that the result was not available.

TABLE 12

F(ab)'$_2$	762 S/S	762 S/F	762 F/F	STOP-1 binding
S7	35nM	4.7nM	2.7nM	Short form
S16	114nM	n/a	32nM	Short form
F5	ND	1uM	N/A	Full length

Fab	762 S/S	762 S/F	762 F/F	STOP-1 binding
S4	3nM	719nM	0.9nM	Short form
S9	>1uM	331nM	N/A	Short form
F13	3.8nM	795nM	n/a	Short form
F47	3.8nM	795nM	n/a	Short form

These antibodies also recognized human STOP-1 in immunoprecipitations.

Example 18 - 6B12 Blocking Assay

The binding location of certain F(ab)'$_2$-phage was also explored. It is known that the monoclonal anti-human STOP-1 antibody, 6B12, binds to an N-terminal region of human STOP-1 protein. Therefore, it was tested whether 6B12 could block binding of certain F(ab)'$_2$-phage to STOP-1.

The 6B12 blocking assay was conducted as follows: 96-well Nunc Maxisorp plates were coated with full length human STOP-1 (2ug/ml in PBS) at 4°C overnight or at room temperature for 2 hours. The wells were blocked by adding 65ul 1% BSA at room temperature for 30 minutes followed by 40ul 1% Tween20 for another 30 minutes. Next, the wells were washed with PBS - 0.05% Tween20 5 times. Various concentrations of 6B12 antibody (in ELISA buffer) were incubated in the wells for 30 minutes at room temperature. Then, S7-F(ab)'$_2$-phage, S16-F(ab)'$_2$-phage or F5-F(ab)'$_2$-phage were added to each well for 10 minutes at a concentration that would normally produce 90% binding capacity in the absence of the 6B12 antibody. The wells were washed with PBS - 0.05% Tween20 5 times.

Binding was quantified by adding 75ul/well of horse radish peroxidase (HRP)-conjugated anti-M13 antibody in PBS plus 0.5%BSA and 0.05% Tween20 at room temperature for 30 minutes (Sidhu et al., supra). The wells were washed with PBS - 0.05% Tween20 at least five times. Next, 100ul/well of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) Peroxidase substrate and Peroxidase Solution B (H_2O_2) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) was added to the well. The reaction was stopped by

adding 100ul 1M Phosphoric Acid (H_3PO_4) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) to each well and allowed to incubate for 5 minutes at room temperature. The OD of the yellow color in each well was determined using a standard ELISA plate reader at 450 nm.

TABLE 13

F(ab)'$_2$	6B12 blocking
S7	-
S16	-
F5	+

Table 13 shows the 6B12 antibody was able to block F(ab)'$_2$-F5 phage but not F(ab)'$_2$-S7 phage or F(ab)'$_2$-S16 phage. Therefore, F5 binds to human STOP-1 in the same N-terminal region as 6B12 whereas S7 and S16 do not.

Example 19 - F(ab) and IgG protein constructs and Protein Expression

F(ab) Constructs for Expression in Bacterial Cells: V0350-2b-S4 and V0350-2b-S7 phagemids were modified by removing the viral cP3 sequences, replacing them with a terminator sequence containing 5'-GCTCGGTTGCCGCCGGGCGTTTTTTATG-3' (SEQ ID NO:85), and removing the sequences encoding the leucine zipper and gD tags (hereinafter, pv0120-S4 and pV0120-S7, respectively). FIG.24C is a schematic of this vector. The pv0120 vectors were transformed into E coli 34B8 cells. Single colonies were picked and grown in complete CRAP medium with 25ug/ml carbenicillin at 30°C for at least 22 hours. The expressed proteins were purified through a Protein G high trap column (Amersham Pharmacia).

Amino acid and nucleic acid sequences coding for an S4-Fab are illustrated in FIGs.32A-G.

IgG Constructs for Expression in Mammalian Cells:

Generally, IgG1 constructs were made by swapping the light chain encoded in the LPG3 vector with the light chain of S4 or S7 and by swapping the V_H and C_H1 region encoded in the LPG4 vector with the V_H and C_H1 region of S4 or S7. FIG.24D is a schematic of the LPG3 and LPG4 vectors encoding the light and heavy chains, respectively, of an IgG

protein. The LPG3 vector encodes a humanized MaE11 E27 light chain. The LPG4 vector encodes a humanized MaE11 E27 heavy chain. Together, they encode a full-length human IgG1 version of humanized MaE11 E27 (an anti-IgE antibody). See, United States Patent 6,172,213 (Lowman) for more information about humanized MaE11 E27. The LPG3 and LPG4 vectors were pRK vectors (Gorman, CM et al., (1990) *DNA Protein Eng. Tech.* 2:3) that were modified by, among other things, inserting the full-length light chain and heavy chain, respectively, of a humanized MaE11 E27. The LPG3 and LPG4 vectors were obtained from Yan Wu at Genentech, Inc., South San Francisco, CA.

The LPG4 vector was digested with BsiwI and ApaI to remove the heavy chain variable regions of the humanized MaE11 E27 antibody. The removed sequences were replaced with a Bsiw1-ApaI fragment from the pv0120-S4 or the pv0120-S7 vectors. The LPG3 vector was digested with EcorRV and KpnI to remove the light chain variable regions of the humanized MaE11 E27 antibody. The removed sequences were replaced with an EcorRV -KpnI fragment from the pv0120-S4 or the pv0120-S7 vectors encoding the light chain variable regions of S4 and S7. The resulting vectors, LPG3-humankappaG6 and LPG4-humanHC-S4, are described in FIGs.35 and 36 (SEQ ID NO:110 and SEQ ID NO:112, respectively). The sequence of LPG4-humanHC-S7 is the same as the sequence of LPG4-humanHC-S4, except that the sequence between the Bsiw1-ApaI sites is the same as the sequence between the Bsiw1-ApaI sites of the pv0120-S7 vector.

LPG3-humankappaG6, LPG4-humanHC-S4 and LPG4-humanHC-S7 dsDNA were prepared for transfection. DP12 DHFR+ CHO cells (ATCC) were seeded at 1.5×10^6 cells/ml in tissue culture media containing 1X Tris EDTA (TE), 2 mg/L insulin, 1% dFBS, 0.15g/L gentamycin sulfate. The cells were incubated at 37°C for one to two hours before transfecting. Next, 3.5L of warm tissue culture media was added to the culture together with 20 mg DNA, 20ml of DMRIE-C reagent (1,2-dimyristyloxypropyl-3-dimethyl-hydroxyl ethyl ammonium bromide, Genentech, Inc.) and incubated for at least more 20 minutes at 37°C. The culture was added to a bioreactor, and 250ml/L of warm tissue culture media was added. The cell culture temperature was shifted to 33°C. After 7-12 days, the cells were centrifuged at 1000rpm for 5 minutes and then the supernatant was filtered through a 0.2um filter. The proteins in the supernatant were purified through a Protein G high trap column (Amersham Pharmacia).

Amino acid and nucleic acid sequences coding for an S4 IgG protein are illustrated in FIGs.33A-F and FIGs.24A-G.

Example 20 - Affinity Measurement of S4 and S7 Fab and IgG

ELISA assays were performed to determine the affinity of S4 and S7 Fab and IgG for human STOP-1. First, the concentration of purified Fab and IgG that would be optimal for use in a competition ELISA assay was determined (i.e., approximately 90% of maximal binding capacity on the coated plate). 96-well Nunc Maxisorp plates were coated with full length or short form human STOP-1 (2ug/ml in PBS) at 4°C overnight or at room temperature for 2 hours. The wells were blocked by adding 65ul 1% BSA for 30 minutes followed by 40ul 1% Tween20 for another 30 minutes. Next, the wells were washed with PBS - 0.05% Tween20 5 times. Concentrations of F(ab) or IgG from 0.1nM to 100nM diluted in ELISA buffer (PBS - 0.5%BSA and 0.05% Tween20) were added to the wells for 15 minutes at room temperature. The wells were then washed with PBS - 0.05% Tween20 at least three times. 75ul of HRP-conjugated Protein G antibody (Amersham, 1/5000 dilution with ELISA buffer) per well was added and incubated at room temperature for 30 minutes. The wells were washed again with PBS - 0.05% Tween20 at least five times. Next, 100ul/well of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) Peroxidase substrate and Peroxidase Solution B (H_2O_2) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) was added to the well. The reaction was stopped by adding 100ul 1M Phosphoric Acid (H_3PO_4) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) to each well and allowed to incubate for 5 minutes at room temperature. The optical density of the color in each well was determined using a standard ELISA plate reader at 450 nm. The dilutions of Fab or IgG were plotted against the O.D. readings.

FIG.19 shows an example of a ELISA assay used to determine the optimal concentration of Fab or IgG in a competition assay. "S coated" refers to a short form (#94-243) of STOP-1 coated on a microtiter plate. "F coated" refers to a full-length form of human STOP-1 coated on a microtiter plate. Approximately 90% of maximal binding was considered to be optimal for use in a competitive ELISA assay.

Next, a competition ELISA was performed using the optimal concentration of Fab and IgG determined above. 96-well Nunc Maxisorp plates were coated with full length or short form human STOP-1 (2ug/ml in PBS) at 4°C overnight or at room temperature for 2 hours. The wells were blocked by adding 65ul 1% BSA for 30 minutes followed by 40ul 1% Tween20 for another 30 minutes. The wells were washed with PBS - 0.05% Tween20 5 times. Based on the binding assay above, 50ul of the dilution of Fab or IgG that resulted in about 90% of maximum binding to the coated plate was incubated with 50ul of various concentrations of full length or short form human STOP-1 (0.1 to 500nM) in ELISA buffer

solution for 1 hour at room temperature in a well. The unbound Fab or IgG was assayed by transferring 75ul of the well mixture to second 96-well plate pre-coated with full length or short form human STOP-1 and incubating at room temperature for 15 minutes. The wells of the second plate were washed with PBS - 0.5% Tween20 at least three times. 75ul of HRP-conjugated Protein G (1/5000 dilution with ELISA buffer) per well was added and incubated at room temperature for 30 minutes. The wells were washed again with PBS - 0.05% Tween20 at least five times. Next, 100ul/well of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) Peroxidase substrate and Peroxidase Solution B (H_2O_2) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) was added to the well. The reaction was stopped by adding 100ul 1M Phosphoric Acid (H_3PO_4) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) to each well and allowed to incubate for 5 minutes at room temperature. The optical density of the color in each well was determined using a standard ELISA plate reader at 450 nm. The concentrations of the added competitor STOP-1 were plotted against the O.D. readings. The IC50 is the concentration of STOP-1 that inhibited 50% of the Fab or IgG binding. See FIG.20A and B. The binding affinities are indicated in the parentheticals.

FIG.21 is a summary of the binding affinities of several phage-derived antibodies against STOP-1. "S/S" refers to an ELISA in which the microtiter plate was coated with a short form of STOP-1 and competed with a short form of STOP-1. "F/S" refers to an ELISA in which the microtiter plate was coated with a full-length form of human STOP-1 and competed with a short form of human STOP-1. "F/F" refers to an ELISA in which the microtiter plate was coated with a full-length form of STOP-1 and competed with a full-length form of STOP-1. The phage used in these studies were the S4-Fab phage and the S7-F(ab)'$_2$ phage.

Example 21 - S4 Blocking Assay

S4 IgG was used in a competitive ELISA assay to see if it could block S4 (Fab)-phage, S7 (F(ab)'$_2$)-phage, S9 (Fab)-phage, S16 (F(ab)'$_2$)-phage or F5 (F(ab)'$_2$)-phage binding to a short form or a full-length form of human STOP-1.

First, 96-well Nunc Maxisorp plates were coated with full length human STOP-1 (2ug/ml in PBS) at 4°C overnight or at room temperature for 2 hours. The wells were blocked by adding 65ul 1% BSA for 30 minutes followed by 40ul 1% Tween20 for another 30 minutes. Next, the wells were washed with PBS - 0.05% Tween20 5 times. Various concentrations of S4 IgG (in ELISA buffer) were incubated in the wells for 30 minutes at room temperature. Then, S4 (Fab)-phage, S7 (F(ab)'$_2$)-phage, S9 (Fab)-phage, S16 (F(ab)'$_2$)-

phage or F5 (F(ab)'$_2$)-phage were added to different wells for 10 minutes at a concentration that would normally produce 90% binding capacity in the absence of the S4 IgG antibody. The wells were washed with PBS - 0.05% Tween20 5 times.

Binding was quantified by adding 75ul/well of horse radish peroxidase (HRP)-conjugated anti-M13 antibody in PBS plus 0.5%BSA and 0.05% Tween20 at room temperature for 30 minutes (Sidhu et al., supra). The wells were washed with PBS - 0.05% Tween20 at least five times. Next, 100ul/well of a 1:1 ratio of 3,3',5,5'-tetramethylbenzidine (TMB) Peroxidase substrate and Peroxidase Solution B (H_2O_2) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) was added to the well. The reaction was stopped by adding 100ul 1M Phosphoric Acid (H_3PO_4) ((Kirkegaard-Perry Laboratories (Gaithersburg, MD)) to each well. The OD of the yellow color in each well was determined using a standard ELISA plate reader at 450 nm.

FIG.22 shows that most of the phage-derived antibodies, except F5, bound a similar region on STOP-1 as the S4 phage-derived antibody. The Y axis refers to percentage unblocked as calculated by dividing the OD450nm value of the well that blocked S4 IgG by the OD450nm value of a well without S4 IgG. The phage tested were S4 (Fab) phage, S7 (F(ab)'$_2$) phage, S9 (Fab) phage, S16 (F(ab)'$_2$) phage and F5 (F(ab)'$_2$) phage. A lower % means the more blocking by S4 IgG.

Example 23 - - Optimizing Binding By Altering The Light Chain Sequence

Binding of the antibodies can be further optimized by, *inter alia*, by altering the sequence of the light chain. Optimization can be carried out by methods known in the art, including known phage display methods. Additionally, the sequence of the light chain CDR's can be changed by site-directed mutagenesis and screened by ELISA assays similar to the methods described in Example 16 above, except that the diversity is generated in the light chain variable region as described in United States Provisional Patent No. 60/385,388, filed June 3, 2002. See also below.

According to one example, the libraries of antibody variable light chain domains are optimized to maximize diversity in the CDR regions while minimizing structural perturbations in the antibody variable domains. Structural perturbations in antibody variable domains are generally associated with improperly folded antibody domains resulting in low yield, for example when produced in bacterial cells. Low yields decrease the number of binders detected in screening. Diversity in the light chain CDR regions can be generated by

identifying solvent accessible and highly diverse positions in each CDR for CDRs L1, L2, L3, and designing an oligonucleotide comprising at least one tailored (i.e., non-random) codon set encoding variant amino acids for the amino acid position corresponding to the position of at least one solvent accessible residue at a highly diverse position in at least one CDR region. A tailored codon set is a degenerate nucleic acid sequence that preferably encodes the most commonly occurring amino acids at the corresponding positions of the solvent accessible residues in known, natural antibodies.

Solvent accessible residues in the CDRs can be identified in the antibody variable domain template molecule by analyzing the crystal structure of the template molecule. Humanized antibody 4D5 is efficiently produced and properly folded when produced in a variety of host cells, including bacterial cell culture. The crystal structure for the humanized antibody 4D5 variable region is known and publicly available at http://www.rcsb.org (accession code IFVC).

The solvent accessible positions in the CDRs of the light chain have been identified using the Insight II program (Accelrys, San Diego, CA).

CDR residues were also analyzed to determine which positions in the CDRs were highly diverse. Highly diverse positions in the CDR regions for the heavy and light chains were identified by examining the sequences of known, naturally occurring antibodies in the Kabat database (Kabat, E.A., et al., (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, NIH Publication No. 91-3242). The Kabat database is also available through http://www.bioinf.org.uk/abs/. In the Kabat database, there were about 1540 sequences of the human light chain and 3600 sequences for the human heavy chain. The CDR sites were aligned and numbered as described by Kabat (see http://www.bioinf.org.uk/abs/du). Highly diverse amino acid positions were identified by lining up and ranking the amino acid usage, from most frequently used to less frequently used for each CDR residue. For example, L3-91 (i.e., residue 91 of the light chain CDR3) was found to be Y (tyrosine) in 849 out of 1582 antibody sequences in the Kabat database, and it is the amino acid found most frequently at this position. Next on the list of frequency serine (occurring in 196 sequences), followed by arginine (169 sequences), alanine (118 sequences), glycine (61 sequences), histidine (41 sequences), with the remaining 35 sequences being one of the remaining amino acids. The frequency of amino acids in human antibody light chain sequences from the Kabat database (including illustrative diverse sites, with corresponding diversity list of amino acids) is shown in FIG.35.

Amino acid residues found in a particular position that collectively constitute the most frequently occurring amino acids among the known, natural antibody sequences can be selected as the basis for library design. The most frequently occurring amino acids were deemed to be those that most commonly found in the top 90% of the list of diverse amino acids (this group of amino acids is referred to herein as "target group of amino acids"). However, as described herein, the percent cutoff for a target group of amino acids can be varied, as described above, according to the circumstances and purpose of the diversity library that is to be achieved.

For humanized antibody 4D5, the positions identified as solvent accessible and highly diverse were:

Light Chain

CDR1	28, 29, 30, 31, 32
CDR2	50, 53
CDR3	91, 92, 93, 94, 96

Heavy Chain

CDR 1	28, 30, 31, 32, 33
CDR2	50, 52, 53, 54, 56, 58

Examples of amino acids that occur at high frequency in natural diversity (i.e., among known, natural antibody sequences) (referred to as "target group" or "natural diversity" in Figure 3), and the designed diversity of amino acids by DNA codons ("Diversity<DNA codon>") for each of these positions is shown in FIG.36.

Codon sets encoding a specific group of amino acids (Diversity) have been designed to include at least a certain percentage of the amino acids in the known, natural sequences (designated as "% covering" in FIG.36). Of the amino acids encoded by a codon set, at least about 40% of the amino acid can target amino acids identified for a particular solvent accessible and highly diverse position (designated as "% good" in FIG.36; amino acids encoded by a codon set that are target amino acids are shown in bold in column 3 of FIG.36). However, as described herein, the % good value can be varied according to circumstance and objectives. The codon sets were selected such that they preferably encoded the amino acids with the highest occurrences at a particular position. The number of non-target amino acids coded by a codon set for a particular position was minimized. Effectiveness of codon set selection/design was evaluated in part based on the "% good" value. A high percentage meant very low non-target amino acids; a high value of "% good" was deemed more

important than having more target amino acids among the amino acids coded by a particular codon set. Redundancy was included in calculating the "% good" value. For evaluation purposes, the "% covering" value was also calculated. This value represents the percentage of natural diversity covered by the "good" amino acids (of the amino acids encoded by a particular codon set). For example, for L3-91, when codon set KMT is used, the "good" amino acids are YSA, which is 75% of the YSAD amino acids encoded by the codon. YSA are amino acids that cover 1190 out of 1580 known, natural antibody sequences at this amino acid position. 1190/1580 equals 75%, which is the "% covering" value. Thus, in one design using KMT at L3-91, 75% of the library covers 75% of the natural diversity in CDRL3 at position 91.

The codon sets were also designed to exclude, when possible, cysteine and stop codons. The presence of cysteine residues tends to cause folding problems and stop codons can decrease the effective library size. In the design of the codon sets, it was also deemed desirable to minimize the number of nontarget amino acids.

The codon sets designed for each solvent accessible and highly diverse residue of humanized antibody 4D5 are shown in FIG.36. At any particular residue, one or more codon set(s) could be used depending on the target amino acids that are identified. For example, two L1 oligonucleotides can be combined - - one containing codon YKG and the other containing TWT at L3-96, or one containing codon DGG and the other containing DHT at H2-50.

The various codon sets could be used to generate diverse libraries with diversity in one or more CDR regions, including CDR L1, CDR L2, CDR L3. For example, FIGs.37-40 show various illustrative versions of codon set designs that can be used to generate diversity. FIG.36 provides a summary of the amino acid coverage of these designs. In general, it is preferable, but not necessary, that the designs narrow the diversity to cover more of the natural diversity and exclude as much as possible the "non-target" amino acids. In some embodiments, a design that does not score the highest based on these criteria can be used to obtain good binders for a STOP-1.

Example 24 - STOP-1 binds to the cell surface of cells

HT1080 cells were incubated with recombinant purified full length human His-tagged STOP-1 (10ug/ml, A; 0.5 million cells per sample) in the presence of 100ug/ml of S7 or 6b12 monoclonal antibodies in FACS buffer (20 mM HEPES, pH 7.5, 140 mM NaCl, 1 mM

CaCl2, 1 mM MgCl2, 2 % FBS) at 4°C for 1 hour. Protein binding was detected by treating the cells with FACS with anti-His monoclonal antibodies (5mg/ml) or anti-Flag (5mg/ml, as a negative control) and followed by FITC-conjugated goat anti-mouse antibodies.

FIG.41 shows that STOP-1 binds specifically to the surface of human HeLa cells, human HT1080 fibroblast cells and human umbilical vein endothelial cells (HUVEC) cells, but not human embryonic kidney 293 cells. It is believed that a receptor for STOP-1 exists on HeLa, HT1080 and HUVEC cells.

Example 25 - S7 monoclonal antibody promotes STOP-1 binding to cells

HT1080 cells were incubated with recombinant purified full length human His-tagged STOP-1 (10ug/ml, A; 0.5 million cells per sample) in presence of 100ug/ml of S7 or 6b12 monoclonal antibodies in FACS buffer (20 mM HEPES, pH 7.5, 140 mM NaCl, 1 mM CaCl2, 1 mM MgCl2, 2 % FBS) at 4°C for 1 hour. Protein binding was detected by FACS treatment with anti-His monoclonal antibodies (5mg/ml) or anti-Flag (5mg/ml, as a control) followed by treatment with FITC-conjugated goat anti-mouse antibodies.

FIG.42 shows that the S7 antibody potentiated STOP-1 binding to the cell surface of HT1080 cells whereas 6B12 did not. The S4 antibody was also tested in the same assay and found to potentiate STOP-1 binding to HT1080 cells. Because the S7 antibodies and S4 antibodies were able to bind to STOP-1 bound to cells, the binding of S7 antibody or S4 antibody to STOP-1 does not appear to interfere with the binding of the STOP-1 receptor to STOP-1. Thus, the epitope that the S7 antibody binds to on STOP-1 does not appear to be required for STOP-1 binding to its receptor.

Example 26 - STOP-1 promotes endothelial cell migration

Directional cell migration was measured using a modified Boyden chemotaxis chamber (Transwells™, Corning, Inc.). Polycarbonate filters with 8 micron pores were incubated with a 0.1% solution of collagen I from Collaborative Sciences overnight at 4°C. This process coated the undersurface of the filters with collagen, an extracellular matrix protein necessary for cell attachment. The next day, the filters were rinsed in PBS and blocked for 1 hr at room temperature with a blocking medium (200 microliters in each lower chamber) that consisted of basic endothelial cell medium (Clonetics) with 1% bovine serum albumin (BSA).

HUVEC cells (from Clonetics, grown in complete medium) were harvested using a cell dissociation solution (0.25% EDTA) and resuspended in a migration medium (endothelial cell basic medium having 0.1% BSA, but no growth factors). The resuspended cells were placed in the upper chamber of the modified Boyden chamber (10,000 cells/ml, 150 microliters/ well). The migration medium containing bFGF (1ng/ml or 10ng/ml, final concentration) or STOP-1 (1ug/ml or 10ug/ml, final concentration) were added to the lower chamber of the modified Boyden chamber (300 microliters/well). Migration medium alone (without bFGF or STOP-1) was added to the lower chambers as controls. Each condition was done in triplicate. The modified Boyden chemotaxis chambers were placed in an incubator at 37°C (5% CO_2) for 3 hours.

Afterwards, cells that had not migrated (located on the top of the filters facing the upper chamber) were gently removed using cotton swabs. The filters were fixed in a 4% paraformaldehyde solution (10 min, RT) and stained with a 0.2 % crystal violet solution (5 min, RT), to visualize the cells. The cells located on the undersurface of the filters (i.e., that migrated) were then counted using a Nikon inverted microscope. The filters were randomized ("blinding" the investigator to the conditions). The cells in six random fields (40x) per filter were counted, 3 filters per condition. The data in FIG.44 represents the mean number of cells from one representative experiment (out of 3).

FIG.43 indicates that STOP-1 is chemotactic (i.e., induces directional migration) to HUVEC cells. This effect is comparable in magnitude to that of bFGF (a growth factor which has been previously shown to induce HUVEC migration and to act overall as a pro-angiogenic molecule). Treatment with both bFGF and STOP-1 did not show an additive effect. Nor did treatment with bFGF or STOP-1 potentiate each other's effects. This preliminary data suggests that STOP-1 acts as a pro-angiogenenic or pro-vasculogenic molecule. Work to further confirm this effect will include the repetition of the same or similar experiment using an antibody that blocks of the interaction of STOP-1 with HUVEC cells.

<u>Example 27 - STOP-1 binds to MDA435 cells</u>

MDA-MB-435 human mammary carcinoma cells were removed from culture flasks with 10 mM EDTA and resuspended in cold PBS containing 2% fetal bovine serum. The cell number was adjusted to 1,000,000 cells/ml, and 0.5 ml of the suspension was dispensed into tubes with 10 mg/ml flag-tagged full length human STOP-1 and 100 mg/ml of specific (6B12) or control (4B7) antibodies. The mixture was incubated for 1 hour on ice and washed

with cold suspension buffer. The mixture was then incubated with anti-flag M2-FITC for 1 hour on ice. Cells were washed in suspension buffer and fluorescence was measured by flow cytometry.

FIG.44 graphically depicts the flow cytometry analysis. The geometric mean value of the signal intensity produced by cells treated with detection antibody alone (anti-flag M2 - FITC antibody without STOP-1) was approximately 7.99. The geometric mean values of the signal intensities produced by the cells treated with STOP-1 alone, STOP-1 with 6B12 and STOP-1 with 4B7 were approximately 13.24, 8.3 and 11.39, respectively. The results show that STOP-1 binds to MDA-MB-435 breast carcinoma cells and that 6B12, a monoclonal antibody specific to STOP-1, blocks STOP-1 binding to those cells. The isotype control, 4B7 antibody, showed no appreciable activity. S4 and S7 antibodies were also used in this assay. Both antibodies did not block STOP-1 from binding to MDA-MB-435 cells, their presence in the assay resulted in an increase in the STOP-1 binding to the cells.

Example 28 - STOP-1 mRNA expression is upregulated by TNFalpha and cellular stress

Previous studies have shown that conditions of low oxygen (hypoxia) or cellular stress promote tumorigenesis and angiogenesis. TNFalpha is often used to stimulate cellular responses associated with stress and has been implicated in promoting angiogenesis and tumorigenesis. To test whether STOP-1 expression was influenced by tumorigenic and angiogenic triggers, HUVEC cells were subjected to treatment with TNFalpha and hypoxic conditions.

HUVEC cells were incubated for 3, 8 or 24 hours with 100ng/ml of human recombinant TNFalpha (Genentech, Inc.) under hypoxic conditions (95% air, 5 %CO2) or normoxic conditions (approximately, 95% air, 5% CO2). The mRNA from the treated cells was extracted and subjected to TaqMan RT-PCR reactions using the primers and conditions described in Example 2. The fold change in expression of STOP-1 mRNA at the end of each time period was calculated by comparing it to its level of expression after three hours of incubation under normoxic conditions (without 100ng/ml TNFalpha).

FIG.45B shows that STOP-1 mRNA expression is significantly upregulated upon treatment with TNFalpha under normoxic conditions. The expression levels did not appear to change substantially at the 3, 8 and 34 hour time points. FIG.45A, on the other hand, shows that TNFalpha has little or no effect on STOP-1 mRNA levels in cells incubated under hypoxic conditions. Interestingly, in absence of TNFalpha, STOP-1 expression was significantly upregulated after 34 hours of treatment under hypoxic conditions, but not after 3

hours of treatment. These results indicate that STOP-1 expression in HUVEC cells is responsive to treatment with TNFalpha and hypoxic conditions, but the response is not additive or synergistic, possibly indicating similar pathways of action.

SEQUENCE LISTING KEY

SEQ ID	Description
1	DNA76393-1664
2	amino acid sequence of DNA76393-1664
3	alternative STOP-1 amino acid sequence
4	mouse STOP-1 amino acid sequence
5	rice fish STOP-1 amino acid sequence
6	zebra fish STOP-1 amino acid sequence
7	chicken STOP-1 amino acid sequence
8	S7 - first amino acid sequence
9	S7 - second amino acid sequence
10	S7 - third amino acid sequence
11	S16 - first amino acid sequence
12	S16 - second amino acid sequence
13	S16 - third amino acid sequence
14	F5 - first amino acid sequence
15	F5 - second amino acid sequence
16	F5 - third amino acid sequence
17	S4 - first amino acid sequence
18	S4 - second amino acid sequence
19	S4 - third amino acid sequence
20	S9 - first amino acid sequence
21	S9 - second amino acid sequence
22	S9 - third amino acid sequence
23	RT-PCR hybridization probe
24	RT-PCR forward primer

25	RT-PCR reverse primer
26	Template sequence
27	Primer sequence
28	Primer sequence
29	Primer sequence
30	Primer sequence
31	Primer sequence
32	Primer sequence
33	Primer sequence
34	Primer sequence
35	Primer sequence
36	Primer sequence
37	Primer sequence
38	Primer sequence
39	Primer sequence
40	Primer sequence
41	Primer sequence
42	Primer sequence
43	Primer sequence
44	Primer sequence
45	Primer sequence
46	Primer sequence
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68	Primer sequence
69	Primer sequence
70	Primer sequence
71	Primer sequence
72	Primer sequence
73	Primer sequence
74	Primer sequence
75	Primer sequence
76	Primer sequence
77	Primer sequence
78	Primer sequence
79	Primer sequence
80	Primer sequence
81	Primer sequence
82	Primer sequence
83	Primer sequence
84	GCN4 leucine zipper
85	Oligo containing terminator sequence
86	an amino acid sequence comprising an anti-Her-2 Fab light chain
87	an amino acid sequence comprising an anti-Her-2 Fab light chain region

88	a nucleic acid sequence of a phagemid encoding SEQ ID NOs: 86 and 87 (pv0350-2b)
89	an amino acid sequence comprising an anti-Her-2 $F(ab)'_2$ light chain
90	an amino acid sequence comprising an anti-Her-2 $F(ab)'_2$ heavy chain region
91	a nucleic acid sequence of a phagemid encoding the amino acid sequences of SEQ ID NOs:89 and 90 (pv0350-4)
92	an amino acid sequence comprising an S4-Fab light chain
93	an amino acid sequence comprising an S4-Fab heavy chain region
94	a nucleic acid sequence encoding the amino acid sequences of SEQ ID NOs:92 and 93
95	an amino acid sequence comprising an S9-Fab light chain
96	an amino acid sequence comprising an S9-Fab heavy chain region
97	a nucleic acid sequence encoding the amino acid sequences of SEQ ID NOs:95 and 96
98	an amino acid sequence comprising an S7-$F(ab)'_2$ light chain
99	an amino acid sequence comprising an S7-$F(ab)'_2$ heavy chain region
100	a nucleic acid sequence encoding the amino acid sequences of SEQ ID NOs:98 and 99
101	an amino acid sequence comprising an S16-$F(ab)'_2$ light chain
102	an amino acid sequence comprising an S16-$F(ab)'_2$ heavy chain region
103	a nucleic acid sequence encoding the amino acid sequences of SEQ ID NOs:101 and 102
104	an amino acid sequence comprising a F5-$F(ab)'_2$ light chain
105	an amino acid sequence comprising an F5-$F(ab)'_2$ heavy chain region
106	a nucleic acid sequence encoding the amino acid sequences of SEQ ID NOs:104 and 105
107	an amino acid sequence comprising an S4-Fab light chain
108	an amino acid sequence comprising an S4-Fab heavy chain region
109	a nucleic acid sequence of a vector encoding the amino acid sequence if SEQ ID NOs:107 and 108 (pv0120-S4)
110	an amino acid sequence comprising an S4 IgG Light Chain

111	a nucleic acid sequence of a vector encoding the amino acid sequence of SEQ ID NO:110 (LPG3.HumanKappaG6)
112	an amino acid sequence comprising an S4 IgG Heavy Chain
113	nucleic acid sequence of a vector encoding the amino acid sequence of SEQ ID NO:112 (LPG4.HumanHC-S4)
114	Consensus Amino Acid Sequence of FIG.1
115	An H2 consensus sequence
116	An H3 consensus sequence

All patent, applications and publications recited herein are hereby incorporated by reference.